

STIC-Biotech/ChemLib

178944

mej

From: Chan, Christina  
Sent: Tuesday, February 07, 2006 7:28 PM  
To: Basi, Nirmal; STIC-Biotech/ChemLib  
Subject: RE: Rush search for App. #: 10/083,168

Please ~~rush~~ Thanks Chris

Chris Chan  
TC 1600 New Hire Training Coordinator and SPE 1644  
(571)-272-0841  
Remsen, 3E89

STIC/CHEN DIVISION  
FEB - 8 2006

-----Original Message-----

From: Basi, Nirmal  
Sent: Tuesday, February 07, 2006 7:27 PM  
To: Chan, Christina  
Subject: Rush search for App. #: 10/083,168

Thurman I am seeking approval for a RUSH sequence search for an amended case, as indicated below. If approved, could you please forward the search to STIC and cc a copy to me.

Examiner: Nirmal S. Basi  
Art Unit 1646  
Office: Remsen Building, Room 4D68  
Mail Room: Remsen Building, room 4C70

Sequence search:

App. #: 10/083,168  
Result format: Paper.

Title: ENDOGENOUS AND NON-ENDOGENOUS VERSIONS OF HUMAN G PROTEIN-  
COUPLED RECEPTORS

Inventors: Liaw et al

Priority Date: 4/14/97  
Please search:  
i) SEQ ID NOS: 16, 84 and 85

\*\*\*\*\*

Searcher: \_\_\_\_\_  
Searcher Phone: \_\_\_\_\_  
Date Searcher Picked up: \_\_\_\_\_  
Date completed: 2-13-06  
Searcher Prep Time: \_\_\_\_\_  
Online Time: \_\_\_\_\_

\*\*\*\*\*

Type of Search \_\_\_\_\_  
NA# \_\_\_\_\_ AA# \_\_\_\_\_  
S/L: \_\_\_\_\_ Oligomer: \_\_\_\_\_  
Encode/Transl: \_\_\_\_\_  
Structure #: \_\_\_\_\_ Text: \_\_\_\_\_  
Inventor: \_\_\_\_\_ Litigation: \_\_\_\_\_

\*\*\*\*\*

Vendors and cost where applicable \_\_\_\_\_  
STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
QUESTEL/ORBIT: \_\_\_\_\_  
LEXIS/NEXIS: \_\_\_\_\_  
SEQUENCE SYSTEM: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other (Specify): \_\_\_\_\_

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Search issued, commercial and interference databases.

Thanks,  
Nirmal S. Basi

\*\*\*\*\*

Searcher: \_\_\_\_\_  
Searcher Phone: \_\_\_\_\_  
Date Searcher Picked up: \_\_\_\_\_  
Date completed: \_\_\_\_\_  
Searcher Prep Time: \_\_\_\_\_  
Online Time: \_\_\_\_\_

\*\*\*\*\*

Type of Search  
NA# \_\_\_\_\_ AA# \_\_\_\_\_  
S/L: \_\_\_\_\_ Oligomer: \_\_\_\_\_  
Encode/Transl: \_\_\_\_\_  
Structure #: \_\_\_\_\_ Text: \_\_\_\_\_  
Inventor: \_\_\_\_\_ Litigation: \_\_\_\_\_

\*\*\*\*\*

Vendors and cost where applicable  
STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
QUESTEL/ORBIS: \_\_\_\_\_  
LEXIS/NEXIS: \_\_\_\_\_  
SEQUENCE SYSTEM: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other (Specify): \_\_\_\_\_

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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 9, 2006, 00:47:19 ; Search time 214.5 Seconds  
(without alignments)  
632.951 Million cell updates/sec

Title: US-10-083-168-16  
Perfect score: 1614  
Sequence: 1 MNGYNTGSGSLDTPPAIK.....AVAPRAKAKHSQDSLCVTLA 309

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq 21.\*  
1: geneseqp1980s.\*  
2: geneseqp1990s.\*  
3: geneseqp2000s.\*  
4: geneseqp2001s.\*  
5: geneseqp2002s.\*  
6: geneseqp2003as.\*  
7: geneseqp2003bs.\*  
8: geneseqp2004s.\*  
9: geneseqp2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID         | Description        |
|------------|-------|-------------|--------|------------|--------------------|
| 1          | 1614  | 100.0       | 309    | 3 AAY79576 | Aay79576 Human G p |
| 2          | 1614  | 100.0       | 309    | 5 ABG95159 | Abg95159 Human GPC |
| 3          | 1614  | 100.0       | 309    | 6 ABP82002 | Abp82002 Human G p |
| 4          | 1614  | 100.0       | 309    | 7 ADB67656 | Adb67656 Human G p |
| 5          | 1614  | 100.0       | 309    | 8 ADO29394 | Ado29394 Human GPC |
| 6          | 1614  | 100.0       | 309    | 8 ADO78094 | Ado78094 Human GPR |
| 7          | 1614  | 100.0       | 309    | 9 ADV73203 | Adv73203 Human col |
| 8          | 1614  | 100.0       | 309    | 9 AEB15039 | Aeb15039 Human GPR |
| 9          | 1609  | 99.7        | 309    | 5 ABG95172 | Abg95172 Human GPC |
| 10         | 1608  | 99.6        | 309    | 3 AAY69989 | Aay69989 Human rec |
| 11         | 1608  | 99.6        | 547    | 7 ADF70461 | Adf70461 Orphan re |
| 12         | 1606  | 99.5        | 309    | 7 ADF50511 | Adf50511 Human GPC |
| 13         | 1602  | 99.3        | 309    | 3 AAY58645 | Aay58645 Human G-p |
| 14         | 1602  | 99.3        | 309    | 6 ADA84069 | Ada84069 Human GPR |
| 15         | 1602  | 99.3        | 394    | 8 ADO78095 | Ado78095 Human GPR |
| 16         | 1602  | 99.3        | 394    | 8 ADR10454 | Adr10454 Human pro |
| 17         | 1382  | 85.6        | 286    | 8 ADP29765 | Adp29765 Human sec |
| 18         | 1124  | 69.6        | 307    | 8 ADO29395 | Ado29395 Mouse GPC |
| 19         | 402   | 24.9        | 370    | 2 AAW62597 | Aaw62597 Human 7-t |
| 20         | 402   | 24.9        | 370    | 5 ABP61511 | Abp61511 Human NF- |
| 21         | 402   | 24.9        | 370    | 6 ABG73513 | Abg73513 Human p2y |
| 22         | 402   | 24.9        | 370    | 6 ABP81870 | Abp81870 Human G p |
| 23         | 402   | 24.9        | 370    | 7 ADH69286 | Adh69286 Human pur |
| 24         | 402   | 24.9        | 370    | 8 ADF91778 | Adf91778 Human p2y |

|    |       |      |     |            |                    |
|----|-------|------|-----|------------|--------------------|
| 25 | 402   | 24.9 | 370 | 8 ADO29049 | Ado29049 Human nov |
| 26 | 402   | 24.9 | 370 | 8 ADQ88244 | Adq88244 Human 241 |
| 27 | 402   | 24.9 | 370 | 8 ADQ81575 | Adq81575 Human lys |
| 28 | 402   | 24.9 | 370 | 8 ADS84260 | Ads84260 Human G p |
| 29 | 402   | 24.9 | 370 | 9 ADV35123 | Adv35123 Human tra |
| 30 | 402   | 24.9 | 608 | 7 ADF70491 | Adf70491 Orphan re |
| 31 | 401   | 24.8 | 370 | 7 ADH69285 | Adh69285 Human pur |
| 32 | 401   | 24.8 | 370 | 8 ADF91777 | Adf91777 Human p2y |
| 33 | 397   | 24.6 | 370 | 8 ADO29050 | Ado29050 Mouse nov |
| 34 | 392   | 24.3 | 370 | 5 ABP61510 | Abp61510 Human NF- |
| 35 | 390   | 24.2 | 368 | 8 ADS84259 | Ads84259 Human G p |
| 36 | 385   | 23.9 | 327 | 8 ADO29415 | Ado29415 Mouse GpC |
| 37 | 381.5 | 23.6 | 363 | 9 ADW44804 | Adw44804 Human RUP |
| 38 | 381.5 | 23.6 | 363 | 9 AEB20962 | Aeb20962 Human EPA |
| 39 | 379.5 | 23.5 | 363 | 9 AEW44807 | Aew44807 Human RUP |
| 40 | 378.5 | 23.5 | 363 | 9 ADW44802 | Adw44802 Human RUP |
| 41 | 377.5 | 23.4 | 363 | 9 ADW44810 | Adw44810 Human RUP |
| 42 | 377.5 | 23.4 | 363 | 9 ADW44805 | Adw44805 Human RUP |
| 43 | 377.5 | 23.4 | 363 | 9 ADW44814 | Adw44814 Human RUP |
| 44 | 376.5 | 23.3 | 363 | 5 AAU77993 | Aau77993 Human inf |

ALIGNMENTS

RESULT 1  
AAY79576  
ID AAY79576 standard; protein; 309 AA.  
XX AC AAY79576;  
XX AC  
DT 15-AUG-2000 (first entry)  
XX Human G protein coupled receptor GPR35.  
DE  
XX GPR35; G protein coupled receptor; human; NIDDM1;  
XX non-insulin-dependent diabetes mellitus; CAPN10 gene; calpain 10;  
KW diagnosis; therapy.  
KW Homo sapiens.  
XX  
XX Key Location/Qualifiers  
FH Misc-difference 174  
FT /note= "encoded by GCG"  
FT Misc-difference 294  
FT /note= "encoded by AGT"  
XX  
XX WO200023603-A2.  
XX  
XX PD 27-APR-2000.  
XX  
XX PF 21-OCT-1999; 99WO-US024890.  
XX  
XX PR 21-OCT-1998; 98US-0105052P.  
XX 13-MAY-1999; 99US-0134175P.  
XX  
XX (ARCH-) ARCH DEV CORP.  
XX (TEXA ) UNIV OF TEXAS SYSTEM.  
XX  
XX PI Polonsky KS, Horikawa Y, Oda N, Sreenan S, Zhou Y, Otani K;  
XX Hanis CL, Bell GI, Cox NJ;  
XX  
XX DR WPI; 2000-339702/29.  
XX N-PSDB; AAA27485, AAY79574, AAY79576.  
XX  
XX PT Method for screening for type 2 diabetes mellitus comprises detecting a  
XX polymorphism in a calpain encoding nucleic acid segment or a protease-  
XX encoding nucleic acid segment.  
XX Claim 75; Page 237-238; 257pp; English.  
XX  
XX The present sequence is that of the human gene encoding G protein coupled

CC receptor, GPR35 as deduced from a composite cDNA (see AAA27485). The  
 CC sequence of GPR35 is similar to that of a putative purinoceptor P2Y9  
 CC (34.1% identity), suggesting that ATP or other nucleotide is its ligand.  
 CC GPR35 mRNA was detected in all adult and foetal tissues examined with  
 CC relatively higher levels in adult lung, small intestine, colon and  
 CC stomach. In these tissues, there are 2 major transcripts of 2.4 and 4.4  
 CC kb, whereas in skeletal muscle there is a single transcript of 9.4 kb.  
 CC The GPR35 gene is located in a 49,136 bp region (see AAA27475) within the  
 CC N10DM1 region of human chromosome 2. This region also includes the CAPN10  
 CC gene, which encodes a novel calpain-like cysteine protease, designated  
 CC calpain 10. Mutations in the CAPN10 gene are responsible for  
 CC susceptibility to type 2 diabetes. Claimed methods for screening for a  
 CC propensity for type 2 diabetes mellitus are based on detection of a  
 CC polymorphism in a calpain encoding nucleic acid. Methods are also claimed  
 CC for identifying modulators of calpain activity, and using these  
 CC modulators to treat diabetes, in particular through the regulation of an  
 CC insulin secretory response or insulin mediated glucose transport  
 CC  
 CC Sequence 309 AA;  
 SQ  
 Query Match 100.0%; Score 1614; DB 3; Length 309;  
 Best Local Similarity 100.0%; Pred. No. 3.1e-167;  
 Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MNGTYNTCGSSDLTPWPPAIIKGFYAVLVGLVLLGLLNSLALWVFCRMOQWTETRIYMT 60  
 DB 1 MNGTYNTCGSSDLTPWPPAIIKGFYAVLVGLVLLGLLNSLALWVFCRMOQWTETRIYMT 60  
 QY 61 NLAVADLCLLCTLPFVLSRLSDTSPCLQSLQGIYLTNRYSISLVTAIAVDVYAVRH 120  
 DB 61 NLAVADLCLLCTLPFVLSRLSDTSPCLQSLQGIYLTNRYSISLVTAIAVDVYAVRH 120  
 QY 121 PLRARGLSRQAAAVCAVLWLVIGSLVARWLLGIQEGGFCFRTRHNFNSMRPPLG 180  
 DB 121 PLRARGLSRQAAAVCAVLWLVIGSLVARWLLGIQEGGFCFRTRHNFNSMRPPLG 180  
 QY 181 YLPLAVVVFCSLKVVTTALAQRPTDVQAEATRKAAVMWANLLVVFVCFPLHVLTVR 240  
 DB 181 YLPLAVVVFCSLKVVTTALAQRPTDVQAEATRKAAVMWANLLVVFVCFPLHVLTVR 240  
 QY 241 LAVGNACALLETTIRRALYITTSKLSANCCLDACIYYTMAKEFQASALAVAPRAKAHS 300  
 DB 241 LAVGNACALLETTIRRALYITTSKLSANCCLDACIYYTMAKEFQASALAVAPRAKAHS 300  
 QY 301 QDSLCTVTLA 309  
 DB 301 QDSLCTVTLA 309  
 RESULT 2  
 ABG95159  
 ID ABG95159 standard; protein; 309 AA.  
 XX  
 AC ABG95159;  
 XX  
 XX 04-DEC-2002 (first entry)  
 XX  
 XX Human GPCR GPR35.  
 XX  
 XX Human; transmembrane receptor; G-protein coupled receptor; GPCR; allergy;  
 XX hypertension; reflux disease; depression; migraine; schizophrenia; ulcer;  
 XX psychotic disorder; asthma; bronchoepaem; anaesthesia;  
 XX myocardial infarction; MI; stroke; glaucoma; anxiety;  
 XX prostatic hyperplasia; epilepsy; prostate cancer; rhinitis; angina;  
 XX prostatic hypertrophy; receptor.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200268600-A2.  
 XX  
 XX 06-SEP-2002.  
 XX  
 XX 26-FEB-2002; 2002WO-US005625.

XX  
 PR 26-FEB-2001; 2001US-0271913P.  
 XX  
 PA (AREN-) ARENA PHARM INC.  
 XX  
 PI Liaw CW, Chalmers DT, Behan DP, Maciejewski-Lenior D, Leonard JN;  
 PI Lin I, Ortuno D;  
 XX  
 XX WPI; 2002-706980/76.  
 DR N-PSDB; ABS73345.  
 XX  
 PT New human G-protein coupled receptor (GPCR), useful for screening agonist  
 or inverse agonist compounds for treating diseases associated with GPCR.  
 PS Claim 29; Page 128-130; 201pp; English.  
 CC  
 CC The present invention relates to transmembrane receptors, particularly  
 CC endogenous human G-protein coupled receptors (GPCRs), mutant (non-  
 CC endogenous) versions of the GPCRs, and the polynucleotide sequences  
 CC encoding them. The GPCRs are useful for screening agonist or inverse  
 CC agonist compounds for treating diseases associated with GPCR. Diseases  
 CC that can be treated with such compounds include allergies, hypertension,  
 CC reflux disease, depression, migraine, schizophrenia, ulcers, psychotic  
 CC disorders, asthma, bronchoepaem, anaesthesia, myocardial infarction (MI),  
 CC stroke, glaucoma, prostatic hyperplasia, epilepsy, prostate cancer,  
 CC anxiety, prostatic hypertrophy, rhinitis, and angina. The present  
 CC sequence represents an endogenous human GPCR  
 XX  
 SQ Sequence 309 AA;  
 Query Match 100.0%; Score 1614; DB 5; Length 309;  
 Best Local Similarity 100.0%; Pred. No. 3.1e-167;  
 Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MNGTYNTCGSSDLTPWPPAIIKGFYAVLVGLVLLGLLNSLALWVFCRMOQWTETRIYMT 60  
 DB 1 MNGTYNTCGSSDLTPWPPAIIKGFYAVLVGLVLLGLLNSLALWVFCRMOQWTETRIYMT 60  
 QY 61 NLAVADLCLLCTLPFVLSRLSDTSPCLQSLQGIYLTNRYSISLVTAIAVDVYAVRH 120  
 DB 61 NLAVADLCLLCTLPFVLSRLSDTSPCLQSLQGIYLTNRYSISLVTAIAVDVYAVRH 120  
 QY 121 PLRARGLSRQAAAVCAVLWLVIGSLVARWLLGIQEGGFCFRTRHNFNSMRPPLG 180  
 DB 121 PLRARGLSRQAAAVCAVLWLVIGSLVARWLLGIQEGGFCFRTRHNFNSMRPPLG 180  
 QY 181 YLPLAVVVFCSLKVVTTALAQRPTDVQAEATRKAAVMWANLLVVFVCFPLHVLTVR 240  
 DB 181 YLPLAVVVFCSLKVVTTALAQRPTDVQAEATRKAAVMWANLLVVFVCFPLHVLTVR 240  
 QY 241 LAVGNACALLETTIRRALYITTSKLSANCCLDACIYYTMAKEFQASALAVAPRAKAHS 300  
 DB 241 LAVGNACALLETTIRRALYITTSKLSANCCLDACIYYTMAKEFQASALAVAPRAKAHS 300  
 QY 301 QDSLCTVTLA 309  
 DB 301 QDSLCTVTLA 309  
 RESULT 3  
 ABP82002  
 ID ABP82002 standard; protein; 309 AA.  
 XX  
 AC ABP82002;  
 XX  
 XX 04-MAR-2003 (first entry)  
 XX  
 XX Human G protein-coupled receptor GPR35 protein SEQ ID NO:492.  
 DE  
 XX G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;  
 KW G protein-coupled receptor modulator; antibody; immune-related disease;  
 KW growth-related disease; cell regeneration-related disease; AIDS; cancer;  
 KW immunological-related cell proliferative disease; autoimmune disease;

KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;  
KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;  
KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;  
KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;  
KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;  
KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;  
KW ulcer.

OS Homo sapiens.

XX WO200261087-A2.

XX 08-AUG-2002.

XX 19-DEC-2001; 2001WO-US050107.

XX 19-DEC-2000; 2000US-0257144P.

XX (LIFE-) LIFESPAN BIOSCIENCES INC.

XX Burner GC, Roush CL, Brown JP;

XX WPI; 2003-046718/04.

XX N-PSDB; AB242852.

XX New isolated antigenic peptides e.g., for G protein-coupled receptors  
XX (GPCR), useful for diagnosing and designing drugs for treating conditions  
XX in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or  
XX autoimmune diseases.

XX Disclosure; Fig 1; 523pp; English.

XX The present invention describes antigenic peptides (I) comprising: (a)  
XX any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino  
XX acids. Also described: (1) an assay for the detection of a particular G  
XX protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;  
XX and (2) an isolated antibody having high specificity and high affinity or  
XX avidity for a particular GPCR. (1) can be used as GPCR modulators and in  
XX gene therapy. The antigenic peptides for GPCRs are useful in detecting an  
XX antibody against a particular GPCR, and in the production of specific  
XX antibodies. The peptides and antibodies are also useful for detecting the  
XX presence or absence of corresponding GPCRs. The antigenic peptides for  
XX GPCRs and antibodies are useful for diagnosing and designing drugs for  
XX treating immune-related diseases, growth-related diseases, cell  
XX regeneration-related disease, immunological-related cell proliferative  
XX diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,  
XX atherosclerosis, bacterial, fungal, protozoan or viral infections,  
XX osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute  
XX inflammation, allergies, Crohn's disease, diabetes, graft versus host  
XX disease, Parkinson's disease, multiple sclerosis, pain, psoriasis, memory  
XX anxiety, depression, schizophrenia, dementia, mental retardation, memory  
XX loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,  
XX hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or  
XX any other disorder in which GPCRs are involved. The antibodies may be  
XX used in immunoassays and immunodiagnosis. AB242523 to AB242869 encode  
XX GPCR proteins given in ABP81675 to ABP82018, which are used in the  
XX exemplification of the present invention

XX Sequence 309 AA;

Query Match 100.0%; Score 1614; DB 6; Length 309;  
Best Local Similarity 100.0%; Pred. No. 3.1e-167;  
Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNGTYNTCGSSDLTPWPAIKLGFYALVGLVLLVGLLNSLALWVFCRCMQQTETRIYMT 60

Db 1 MNGTYNTCGSSDLTPWPAIKLGFYALVGLVLLVGLLNSLALWVFCRCMQQTETRIYMT 60

QY 61 NLAVADCLLCTLPFVLSLRDSDTLPCLQSLQGIYLTNRYSISLVTAIVDRYVAVRH 120

Db 61 NLAVADCLLCTLPFVLSLRDSDTLPCLQSLQGIYLTNRYSISLVTAIVDRYVAVRH 120

QY 121 PLRAGRLSPRQAACAVLWLVIGSLVARWLLGIQEGGFCFRSTRNFMSPPLGLF 180

Db 121 PLRAGRLSPRQAACAVLWLVIGSLVARWLLGIQEGGFCFRSTRNFMSPPLGLF 180  
QY 181 YLPLAVVVFCSLKVVTALAQRPPTDVGQAEATKRAARMVWNLVVFVVCFLPLHVGLTVR 240  
Db 181 YLPLAVVVFCSLKVVTALAQRPPTDVGQAEATKRAARMVWNLVVFVVCFLPLHVGLTVR 240  
QY 241 LAVGNACALLETIRRALYITSKLSNCCCLDAICYYYMAKEFQESALAVAPRAKAHS 300  
Db 241 LAVGNACALLETIRRALYITSKLSNCCCLDAICYYYMAKEFQESALAVAPRAKAHS 300  
QY 301 QDSLCLVTILA 309  
Db 301 QDSLCLVTILA 309

RESULT 4

ADB67656

ID ADB67656 standard; protein; 309 AA.

XX ADB67656;

DT 04-DEC-2003 (first entry)

DE Human G protein-coupled receptor 35, SEQ ID 25.

KW Cardiant; Gene therapy; heart failure; human;

KW G protein-coupled receptor 35; receptor.

OS Homo sapiens.

XX WO2003072824-A1.

XX 04-SEP-2003.

XX 27-FEB-2003; 2003WO-JP0022228.

XX 28-FEB-2002; 2002JP-00054388.

XX 15-APR-2002; 2002JP-00112228.

XX (SANY ) SANKYO CO LTD.

XX Kitakaze M, Takashima S, Asakura M, Isomura T, Furukawa H;

PI Koishi R, Nakamaru K;

XX WPI; 2003-679959/64.

DR N-PSDB; ADB67672.

XX Predicting pathological conditions in heart failure using marker genes

XX Claim 1; Page 111-113; 137pp; Japanese.

XX The present invention relates to a method for predicting pathological  
XX conditions in heart failure using expression of one of 17 gene sequences  
XX (ADB67663-ADB67678); or protein sequences encoded by the genes (ADB67648-  
XX ADB67662). The proteins and genes are useful for diagnosis, treatment and  
XX prevention of heart failure.

XX Sequence 309 AA;

Query Match 100.0%; Score 1614; DB 7; Length 309;  
Best Local Similarity 100.0%; Pred. No. 3.1e-167;  
Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNGTYNTCGSSDLTPWPAIKLGFYALVGLVLLVGLLNSLALWVFCRCMQQTETRIYMT 60

Db 1 MNGTYNTCGSSDLTPWPAIKLGFYALVGLVLLVGLLNSLALWVFCRCMQQTETRIYMT 60

QY 61 NLAVADCLLCTLPFVLSLRDSDTLPCLQSLQGIYLTNRYSISLVTAIVDRYVAVRH 120

Db 61 NLAVADCLLCTLPFVLSLRDSDTLPCLQSLQGIYLTNRYSISLVTAIVDRYVAVRH 120



XX Homo sapiens.  
XX DE10254601-A1.  
XX  
XX  
XX 03-JUN-2004.  
XX  
XX 22-NOV-2002; 2002DE-01054601.  
XX  
XX 22-NOV-2002; 2002DE-01054601.  
XX  
XX (GANY-) GANYMED PHARM AG.  
XX  
XX Tuereci O, Sahin U, Koslowski M;  
XX  
XX WPI; 2004-421820/40.  
XX  
XX N-PSDB; ADO78086.  
XX  
XX Composition containing inhibitor of expression or activity of specific  
XX tumor-associated antigens, useful for treating cancers, also related  
XX compositions for diagnosis and monitoring.  
XX  
XX Claim 72; SEQ ID NO 9; 124pp; German.  
XX  
XX The invention relates to pharmaceutical compositions that comprise an  
XX agent that inhibits the expression or activity of a tumour-associated  
XX antigen (TAG) that is encoded by a nucleic acid. The pharmaceutical  
XX compositions and related compositions, are used for treatment of diseases  
XX associated with (abnormal) expression of TAG, specifically cancer e.g. of  
XX lung, breast, prostate, colon, stomach, pancreas, ear/nose/throat, kidney  
XX or cervix, also melanoma. Compositions containing TAG, or related nucleic  
XX acid, antibodies or host cells, are also useful for diagnosis and  
XX monitoring of tumours. The present sequence represents the amino acid  
XX sequence of a human GPR35.  
XX  
XX SQ Sequence 309 AA;

Query Match 100.0%; Score 1614; DB 8; Length 309;  
Best Local Similarity 100.0%; Pred. No. 3.1e-167;  
Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNGTNTCGSSDLTPWPAIKLGFYAYLVGLVLLGLLNSLALWVFCRQMQWTETRIYMT 60  
DB 1 MNGTNTCGSSDLTPWPAIKLGFYAYLVGLVLLGLLNSLALWVFCRQMQWTETRIYMT 60

QY 61 NLAVADLCCLCTLPFVLSLSDTSPPLCQLSQGIYLTNRYSISLVTAIAVDVAVRH 120  
DB 61 NLAVADLCCLCTLPFVLSLSDTSPPLCQLSQGIYLTNRYSISLVTAIAVDVAVRH 120

QY 121 PLRARGLSRPROAAAVCAVLWLVIGSLVARWLLGIQEGGFCFRSTRHNFNSMRPPLG 180  
DB 121 PLRARGLSRPROAAAVCAVLWLVIGSLVARWLLGIQEGGFCFRSTRHNFNSMRPPLG 180

QY 181 YLPLAVVFCSLKVVTALAQRPTDVQAEATKAAARMVWVWVFCFLPHVGLTVR 240  
DB 181 YLPLAVVFCSLKVVTALAQRPTDVQAEATKAAARMVWVWVFCFLPHVGLTVR 240

QY 241 LAVGNACALLETTIRRALYITSKLSDANCCDAICYNNMAKEFOEASALAVAPRAKAHKS 300  
DB 241 LAVGNACALLETTIRRALYITSKLSDANCCDAICYNNMAKEFOEASALAVAPRAKAHKS 300

QY 301 QDSLVCVTLA 309  
DB 301 QDSLVCVTLA 309

RESULT 7  
ADV73203  
ID ADV73203 standard; protein; 309 AA.  
XX  
XX AC ADV73203;  
XX  
XX 10-MAR-2005 (first entry)  
DT

XX Human colon tumor cell upregulated protein SEQ ID NO 44.  
XX  
XX cancer; neoplasm; cytostatic.  
XX  
XX Homo sapiens.  
XX OS  
XX WO2004110345-A2.  
XX  
XX 23-DEC-2004.  
XX  
XX 28-OCT-2003; 2003WO-US034019.  
XX  
XX 29-OCT-2002; 2002US-0422176P.  
XX  
XX (PHAA ) PHARMACIA CORP.  
XX  
XX Bourner MJ, Bu JJ, Head RD, Hippenmeyer PJ, Klein BK;  
XX Mazzarella RA, Staten NR;  
XX WPI; 2005-039958/04.  
XX  
XX N-PSDB; ADV73165.  
XX  
XX New antibody that immunospecifically binds to p-cadherin, useful in  
XX preparing a composition for treating or preventing a cancer-associated  
XX disorder.  
XX  
XX Disclosure; SEQ ID NO 44; 257pp; English.  
XX  
XX The invention relates to an antibody immunospecifically binds to p-  
XX cadherin or its fragment. The antibody is useful in preparing a  
XX composition for treating or preventing a cancer-associated disorder. The  
XX present sequence represents the amino acid sequence of a protein  
XX upregulated in human colon cancer cells.  
XX  
XX SQ Sequence 309 AA;

Query Match 100.0%; Score 1614; DB 9; Length 309;  
Best Local Similarity 100.0%; Pred. No. 3.1e-167;  
Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNGTNTCGSSDLTPWPAIKLGFYAYLVGLVLLGLLNSLALWVFCRQMQWTETRIYMT 60  
DB 1 MNGTNTCGSSDLTPWPAIKLGFYAYLVGLVLLGLLNSLALWVFCRQMQWTETRIYMT 60

QY 61 NLAVADLCCLCTLPFVLSLSDTSPPLCQLSQGIYLTNRYSISLVTAIAVDVAVRH 120  
DB 61 NLAVADLCCLCTLPFVLSLSDTSPPLCQLSQGIYLTNRYSISLVTAIAVDVAVRH 120

QY 121 PLRARGLSRPROAAAVCAVLWLVIGSLVARWLLGIQEGGFCFRSTRHNFNSMRPPLG 180  
DB 121 PLRARGLSRPROAAAVCAVLWLVIGSLVARWLLGIQEGGFCFRSTRHNFNSMRPPLG 180

QY 181 YLPLAVVFCSLKVVTALAQRPTDVQAEATKAAARMVWVWVFCFLPHVGLTVR 240  
DB 181 YLPLAVVFCSLKVVTALAQRPTDVQAEATKAAARMVWVWVFCFLPHVGLTVR 240

QY 241 LAVGNACALLETTIRRALYITSKLSDANCCDAICYNNMAKEFOEASALAVAPRAKAHKS 300  
DB 241 LAVGNACALLETTIRRALYITSKLSDANCCDAICYNNMAKEFOEASALAVAPRAKAHKS 300

QY 301 QDSLVCVTLA 309  
DB 301 QDSLVCVTLA 309

RESULT 8  
AEB15039  
ID AEB15039 standard; protein; 309 AA.  
XX  
XX AC AEB15039;  
XX  
XX 08-SEP-2005 (first entry)  
DT



# LE

```
RESULT 11
ADF70461
XX ADF70461 standard; protein; 547 AA.
XX
XX ADF70461;
XX
XX 12-FEB-2004 (first entry)
XX
XX Orphan receptor ligand-related human protein SeqID84.
XX
XX ligand; orphan receptor protein; fusion protein; fluorescent protein;
XX cell expression; green fluorescent protein; GFP; GFP-1; wild-type GFP;
XX GFPuv; Enhanced GFP; EGFP; human.
XX
XX Homo sapiens.
XX
XX WO2003071272-A1.
XX
XX 28-AUG-2003.
XX
XX 21-FEB-2003; 2003WO-JP001901.
XX
XX 22-FEB-2002; 2002JP-00045728.
XX
XX 23-JUL-2002; 2002JP-00213949.
XX
XX 11-OCT-2002; 2002JP-00298237.
XX
XX (TAKA ) TAKEDA CHEM IND LTD.
XX
XX Hinuma S, Fujii R, Ogi K, Komatsu H, Kawamata Y, Hosoya M;
XX WPI; 2003-697654/66.
XX
XX N-PSDB; ADF70563.
XX
XX Transformation of cells with a fusion protein of an orphan receptor
XX PT protein with a fluorescent protein useful for identification of ligands
XX to the orphan receptor.
XX
XX Disclosure; SEQ ID NO 84; 594pp; Japanese.
XX
XX This invention relates to a novel method of identifying ligands to an
XX orphan receptor protein which comprises transforming cells with DNA
XX encoding a fusion protein of the orphan receptor with a fluorescent
XX protein, so that the fusion protein is expressed in the cells (or cell
XX membranes isolated from them) and contacting the cells with the potential
XX ligand to be tested. A suitable fluorescent protein for incorporation in
XX the fusion protein is green fluorescent protein (GFP), for example GFP-1,
XX wild-type GFP, GFPuv or Enhanced GFP (EGFP). The method is useful for the
XX identification of ligands binding to an orphan receptor protein.
XX
XX Sequence 547 AA;
XX
Query Match 99.6%; Score 1608; DB 7; Length 547;
Best Local Similarity 99.7%; Pred. No. 2.8e-166;
Matches 308; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MNGTYNTCGSSDLTPWPPAIKLGFYAYLVGLVLLVGLLNSLALWVFCRMOQWTEIRYMT 60
DB 1 MNGTYNTCGSSDLTPWPPAIKLGFYAYLVGLVLLVGLLNSLALWVFCRMOQWTEIRYMT 60
QY 61 NLAVADLCLLCTLPFFVLSRLDTSPTPLQLSQGIYLTNRYSISLVTAIAVDYVAVRH 120
DB 61 NLAVADLCLLCTLPFFVLSRLDTSPTPLQLSQGIYLTNRYSISLVTAIAVDYVAVRH 120
QY 121 PLRARGLRPRQAAAVCAVLWLVISLVARMLLGIQGGFCFRSTRHNFNSMRPPLG 180
DB 121 PLRARGLRPRQAAAVCAVLWLVISLVARMLLGIQGGFCFRSTRHNFNSMRPPLG 180
QY 181 YLPLAVVVFCSLKVVTALQRPPTDVQAEATRKAAWYMANLLVFWVCFPLHVLTVR 240
DB 181 YLPLAVVVFCSLKVVTALQRPPTDVQAEATRKAAWYMANLLVFWVCFPLHVLTVR 240
QY 241 LAVGNACALLETIRRALYITSKLSANDCLDAICYYYMAKEFQESALAVAPRAKAHKS 300
DB 241 LAVGNACALLETIRRALYITSKLSANDCLDAICYYYMAKEFQESALAVAPRAKAHKS 300
QY 301 QDSLVCVTILA 309
DB 301 QDSLVCVTILA 309
RESULT 12
ADF50511
XX ADF50511 standard; protein; 309 AA.
XX
XX ADF50511;
XX
XX 12-FEB-2004 (first entry)
XX
XX Human GPCR GPR35 D113A mutein (SeqID 191).
XX
XX mutant; mutein; transformation; endocrine cell line;
XX expression cloning system; bioactive peptide; GPCR ligand; human.
XX
XX Synthetic.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX FT Misc-difference 113 /note= "Wild type Asp substituted by Ala"
XX FT
XX WO2003087366-A1.
XX
XX 23-OCT-2003.
XX
XX 16-APR-2003; 2003WO-JP004840.
XX
XX 16-APR-2002; 2002JP-00113030.
XX
XX (KYOW ) KYOWA HAKKO KOGYO KK.
XX
XX Sasaki K, Miura K, Saeki S, Yoshizawa M, Kishimoto K, Kunitomo H;
XX Nishi T, Obinata M;
XX WPI; 2003-833737/77.
XX
XX Endocrine cell lines originated from mammalian hypothalamus and
XX pancreatic islet, applicable in expression cloning systems of bioactive
XX peptide precursor genes, and in screening G protein-coupled receptor
XX ligands.
XX
XX Example 24; SEQ ID NO 191; 316pp; Japanese.
XX
XX This invention relates to a novel method for obtaining a DNA that encodes
XX a peptide acting as agonist, antagonist or inverse agonist on a target
XX receptor. Specifically, it comprises transformation of endocrine cell
XX lines originating from mammalian hypothalamus and pancreatic islets,
XX culturing the transformants and contacting with cells expressing the
XX target receptor. The identification of those cells with a response
XX reaction can be used for selecting a transformant cell line with the
XX appropriate target activity that is expressing the novel transformed DNA.
XX Accordingly, the present invention describes novel cell lines that are
XX applicable in expression cloning systems of bioactive peptide precursor
XX genes, and in screening GPCR ligands for use as drugs including agonists,
XX antagonists and inverse agonists i.e. activators and inhibitors. Such
XX cell lines can provide a highly sensitive and convenient GPCR ligand
XX assay system. This polypeptide sequence is the human GPCR GPR35 D113A
XX mutein of the invention.
XX
XX Sequence 309 AA;
XX
Query Match 99.5%; Score 1606; DB 7; Length 309;
Best Local Similarity 99.7%; Pred. No. 2.3e-166;
Matches 308; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MNGTYNTCGSSDLTPWPPAIKLGFYAYLVGLVLLVGLLNSLALWVFCRMOQWTEIRYMT 60
DB 1 MNGTYNTCGSSDLTPWPPAIKLGFYAYLVGLVLLVGLLNSLALWVFCRMOQWTEIRYMT 60
```



Db 1 MNGYNTCGSDLTWPPAIAKLGFAVYGLVLLVGLLLNSLALWVFCRMOQWTTETRIYMT 60  
Qy 61 NLAVADCLLCTLPVLSHSDTSTPLCOLSQGIYLTNRYSLSLVAIAVDVAVRH 120  
Db 61 NLAVADCLLCTLPVLSHSDTSTPLCOLSQGIYLTNRYSLSLVAIAVDVAVRH 120  
Qy 121 PLRAGLRSPQAAAVCAVAVLWLVIGSLVARWLLGIQEGGFCFRSTRNFNSMRPPLG 180  
Db 121 PLRAGLRSPQAAAVCAVAVLWLVIGSLVARWLLGIQEGGFCFRSTRNFNSMRPPLG 180  
Qy 181 YLPLAVVFCSLKVVTALAQRPPTDVGOAEATRKARVMWANLLVVFVCFPLHVLTVR 240  
Db 181 YLPLAVVFCSLKVVTALAQRPPTDVGOAEATRKARVMWANLLVVFVCFPLHVLTVR 240  
Qy 241 LAVGNACALLETIRRALYITSKLSDANCCLDIAICYTMAKEFQASALAVAPRAKHS 300  
Db 241 LAVGNACALLETIRRALYITSKLSDANCCLDIAICYTMAKEFQASALAVAPRAKHS 300  
Qy 301 QDSLCTVLA 309  
Db 301 QDSLCTVLA 309

## RESULT 13

AAVS8645

ID AAVS8645 standard; protein; 309 AA.

XX AC AAVS8645;

XX DT 11-APR-2000 (first entry)

XX DE Human G-protein coupled receptor GPR35A.

XX KW GPR35A; human; G-protein coupled receptor; purinergic;

XX KW 7-transmembrane receptor; antibiotic; antifungal; antiviral; analgesic;

XX KW cytotatic; antidiabetic; anorectic; antiasthmatic; antiparkinsonian;

XX KW hypertensive; hypertensive; osteopathic; antianal; cardiac;

XX KW cerebroprotective; antiulcer; antiallergic; antimigraine; antiemetic;

XX KW tranquilizer; antidepressant; neuroleptic; nootropic; anticonvulsant;

XX KW therapy; diagnosis; vaccine.

XX OS Homo sapiens.

XX XX WO964452-A1.

XX PD 16-DEC-1999.

XX PF 01-JUN-1999; 99WO-US012123.

XX PR 11-JUN-1998; 98US-00096031.

XX XX (SMIK ) SMITHKLINE BEECHAM CORP.

XX PA Elshourbagy NA;

XX PI Elshourbagy NA;

XX XX WPI; 2000-116525/10.

XX DR N-PSDB; AA235390.

XX XX New human GPR35A polypeptides and polynucleotides used to identify

XX PT agonists, antagonists and inhibitors for use in therapy.

XX PT Claim 1; Page 32-33; 38pp; English.

XX PS

XX XX The present sequence represents human GPR35A, a novel member of the

XX CC purinergic family of polypeptides and a G-protein coupled receptor. The

XX CC invention provides GPR35A polypeptides having at least 70% identity with

XX CC the present sequence, GPR35A polynucleotides, recombinant materials, and

XX CC methods for their production. GPR35A polypeptides can be used for

XX CC identifying agonists and antagonists/inhibitors, and for detecting

XX CC diseases associated with inappropriate GPR35A activity or levels. GPR35A

XX CC polypeptides and polynucleotides, agonists, antagonists and antibodies

XX CC are used to treat: infections such as bacterial, fungal, protozoan and

XX CC viral infections, particularly HIV-1 and HIV-2; pain; cancer; diabetes;

CC obesity; anorexia; bulimia; asthma; Parkinson's disease; acute heart  
CC failure; hypotension; hypertension; urinary retention; osteoporosis;  
CC angina pectoris; myocardial infarction; stroke; ulcers; allergy; benign  
CC prostatic hypertrophy; migraine; vomiting; psychotic and neurological  
CC disorders including anxiety, schizophrenia, manic depression, depression,  
CC delirium, dementia and severe mental retardation; and dyskinesias such as  
CC Huntington's or Gilles de la Tourette's syndrome. The polypeptide is also  
CC useful for production of vaccines

SQ Sequence 309 AA;

Query Match 99.3%; Score 1602; DB 3; Length 309;

Best Local Similarity 99.4%; Pred. No. 6.3e-166;

Matches 307; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MNGYNTCGSDLTWPPAIAKLGFAVYGLVLLVGLLLNSLALWVFCRMOQWTTETRIYMT 60

Db 1 MNGYNTCGSDLTWPPAIAKLGFAVYGLVLLVGLLLNSLALWVFCRMOQWTTETRIYMT 60

Qy 61 NLAVADCLLCTLPVLSHSDTSTPLCOLSQGIYLTNRYSLSLVAIAVDVAVRH 120

Db 61 NLAVADCLLCTLPVLSHSDTSTPLCOLSQGIYLTNRYSLSLVAIAVDVAVRH 120

Qy 121 PLRAGLRSPQAAAVCAVAVLWLVIGSLVARWLLGIQEGGFCFRSTRNFNSMRPPLG 180

Db 121 PLRAGLRSPQAAAVCAVAVLWLVIGSLVARWLLGIQEGGFCFRSTRNFNSMRPPLG 180

Qy 181 YLPLAVVFCSLKVVTALAQRPPTDVGOAEATRKARVMWANLLVVFVCFPLHVLTVR 240

Db 181 YLPLAVVFCSLKVVTALAQRPPTDVGOAEATRKARVMWANLLVVFVCFPLHVLTVR 240

Qy 241 LAVGNACALLETIRRALYITSKLSDANCCLDIAICYTMAKEFQASALAVAPRAKHS 300

Db 241 LAVGNACALLETIRRALYITSKLSDANCCLDIAICYTMAKEFQASALAVAPRAKHS 300

Qy 301 QDSLCTVLA 309

Db 301 QDSLCTVLA 309

## RESULT 14

ADA84069

ID ADA84069 standard; protein; 309 AA.

XX AC ADA84069;

XX XX 20-NOV-2003 (first entry)

XX DT Human GPR35 protein.

XX DE human; marker; expressed sequence tag; EST; arabinidopsis; tumour;

XX KW stress-induced phenotype, hyperosmotic stress; colon cancer; immunogen;

XX KW vaccine.

XX OS Homo sapiens.

XX XX WO2002103028-A2.

XX PN 27-DEC-2002.

XX PF 30-MAY-2002; 2002WO-IB004189.

XX XX 30-MAY-2001; 2001US-0293999P.

XX PR 22-OCT-2001; 2001US-0330457P.

XX PR 19-FEB-2002; 2002US-0357144P.

XX XX (BIOM-) BIOMEDICAL CENT.

XX PI Baranova AV, Yankovsky NK, Kozlov AP, Lobashev AV, Krukovskaya LL;

XX DR WPI; 2003-175241/17.

XX DR N-PSDB; ADA84068.

XX XX



GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: February 9, 2006, 00:55:13 ; Search time 26.5 Seconds  
(without alignments)  
1121.924 Million cell updates/sec

Title: US-10-083-168-16  
Perfect score: 1614  
Sequence: 1 MNGYNTGSGDLTPPAIK.....AVAPRAKHSQDSLCVTLA 309

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 80:\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID     | Description        |
|------------|-------|-------------|--------|--------|--------------------|
| 1          | 401   | 24.8        | 370    | JC5549 | heptahelical P2Y5- |
| 2          | 368.5 | 22.8        | 308    | I50241 | G protein-coupled  |
| 3          | 368.5 | 22.8        | 387    | I69202 | G protein-coupled  |
| 4          | 360.5 | 22.3        | 344    | T09508 | intron 17 purinerg |
| 5          | 319   | 19.8        | 328    | I55450 | G protein-coupled  |
| 6          | 319   | 19.8        | 373    | A47556 | ATP receptor P2u - |
| 7          | 318   | 19.7        | 362    | S33733 | G protein-coupled  |
| 8          | 315.5 | 19.5        | 365    | S68679 | G protein-coupled  |
| 9          | 312.5 | 19.4        | 364    | JQ1488 | bradykinin B2 rece |
| 10         | 312.5 | 19.4        | 366    | OORTB2 | bradykinin recepto |
| 11         | 310   | 19.2        | 342    | S13638 | platelet-activatin |
| 12         | 308.5 | 19.1        | 375    | A54936 | P-2U nucleotide re |
| 13         | 305.5 | 18.9        | 354    | I53033 | G protein-coupled  |
| 14         | 305.5 | 18.9        | 362    | A57641 | G protein-coupled  |
| 15         | 305   | 18.9        | 352    | S60024 | bradykinin B1 rece |
| 16         | 304   | 18.8        | 342    | A40191 | platelet-activatin |
| 17         | 302.5 | 18.7        | 362    | B57641 | G protein-coupled  |
| 18         | 302.5 | 18.7        | 373    | JC4162 | P2Y receptor - bov |
| 19         | 301.5 | 18.7        | 362    | S68207 | G protein-coupled  |
| 20         | 298.5 | 18.5        | 373    | JC4737 | G protein-coupled  |
| 21         | 293   | 18.2        | 341    | S43252 | platelet-activatin |
| 22         | 291   | 18.0        | 328    | JC4800 | P2Y6 receptor - hu |
| 23         | 289   | 17.9        | 363    | JC2543 | angiotensin II rec |
| 24         | 288.5 | 17.9        | 352    | A43113 | chemokine (C-C) re |
| 25         | 285.5 | 17.7        | 361    | B45680 | platelet activatin |
| 26         | 283   | 17.5        | 341    | S63666 | bradykinin B2 rece |
| 27         | 281.5 | 17.4        | 366    | I49519 | somatostatin recep |
| 28         | 279.5 | 17.3        | 363    | I57955 | somatostatin recep |
| 29         | 279.5 | 17.3        | 364    | JN0763 | somatostatin recep |

|    |       |      |     |   |        |                    |
|----|-------|------|-----|---|--------|--------------------|
| 30 | 278   | 17.2 | 363 | 2 | A49092 | angiotensin II rec |
| 31 | 276.5 | 17.1 | 361 | 2 | JC5653 | G protein-coupled  |
| 32 | 275   | 17.0 | 363 | 2 | I48261 | angiotensin II rec |
| 33 | 275   | 17.0 | 363 | 2 | I57940 | somatostatin recep |
| 34 | 272.5 | 16.9 | 355 | 2 | I49339 | macrophage inflam  |
| 35 | 271.5 | 16.8 | 420 | 2 | I51667 | thrombin receptor  |
| 36 | 271   | 16.8 | 354 | 2 | T09353 | G protein-coupled  |
| 37 | 269.5 | 16.7 | 365 | 2 | S68208 | G protein-coupled  |
| 38 | 269   | 16.7 | 323 | 1 | Q0BED3 | HRF3 protein - hu  |
| 39 | 268   | 16.6 | 418 | 2 | A46226 | somatostatin recep |
| 40 | 266.5 | 16.5 | 355 | 2 | JC5067 | G protein-coupled  |
| 41 | 263.5 | 16.3 | 369 | 2 | JC5068 | G protein-coupled  |
| 42 | 262.5 | 16.3 | 355 | 2 | A45177 | chemokine (C-C) re |
| 43 | 262.5 | 16.3 | 391 | 2 | A41795 | somatostatin recep |
| 44 | 262.5 | 16.3 | 391 | 2 | C41795 | somatostatin recep |
| 45 | 262.5 | 16.3 | 391 | 2 | A39297 | somatostatin recep |

ALIGNMENTS

RESULT 1

JC5549  
heptahelical P2Y5-like receptor - human  
C:Species: Homo sapiens (man)  
C:Date: 02-Sep-1997 #sequence\_revision 05-Sep-1997 #text\_change 09-Jul-2004  
C:Accession: JC5549  
R:Janssens, R.; Boeynaems, J.M.; Godart, M.; Communi, D.  
Biochem. Biophys. Res. Commun. 236, 106-112, 1997  
A:Title: Cloning of a human heptahelical receptor closely related to the P2Y5 receptor.  
A:Reference number: JC5549; MUID:97366605; PMID:9223435  
A:Accession: JC5549  
A:Molecule type: DNA  
A:Residues: 1-370 <JAN>  
A:Cross-references: UNIPROT:Q99677; UNIPARC:UPI000016A4CA; DDBJ:AF005419; NID:G2240034;  
C:Superfamily: ATP receptor P2u

Query Match 24.8%; Score 401; DB 2; Length 370;  
Best Local Similarity 34.0%; Pred. No. 1.9e-29;  
Matches 105; Conservative 58; Mismatches 104; Indels 42; Gaps 11;

|    |     |  |     |
|----|-----|--|-----|
| QY | 25  | AYLGVLVLLNSLALWVFCRQQWTEIRIYNTNINLAVADLCCLTLPF-VLHSLR--      | 81  |
| DB | 44  | AVYSVVFILGILTNSVLSLVFVCFRMRSETAIFITNLAVSDLLFVCTLPFKIFYNRHR   | 103 |
| QY | 82  | -DTSPTPLCOLSQGIYLTNRYMSISLVTAIAVDVVAVRHPLRGLRSPROAAAVCAVL    | 140 |
| DB | 104 | WPFQGT-LCKISGTAFLTNIYGSMLFLTCISVDRLAIVIPPRRTITRRNSAIVCAGV    | 162 |
| QY | 141 | WLVITGSLVARWLLGIQGGF-----CFR-----STRHFNMSRFPPLGPLYL          | 182 |
| DB | 163 | WILVLSG-----GISASLFTTNVNNATTCFGLSKRVKTYLSKITIFIEVVGFII       | 215 |
| QY | 183 | PLAVVVVCSLKVVTAQAQPPDVGQABAT-RKAARMVWNLIVFVCPPLHVGTLVRL      | 241 |
| DB | 216 | PLILNVSCSSVVLRTL--RKPATLSQIGTNKKKVLKMITVHMVAVFVCFVPSNVSLFLYA | 273 |
| QY | 242 | AVGNWAC--ALLETTRALY-ITSKLSDNCCLDACIYYMAKEFQESALAVAPRAKAH     | 298 |
| DB | 274 | LVRSQAITNCFERFAKIMYPITCLATLNCDFPFIFYFTLESFQKSFYI-----NAH     | 327 |
| QY | 299 | KSQDSILCVT 307   |     |
| DB | 328 | RMESLFKT 336   |     |

RESULT 2

I50241  
G protein-coupled receptor 6H1 - chicken  
N:Alternate names: purinoceptor 6H1  
C:Species: Gallus gallus (chicken)  
C:Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 09-Jul-2004  
C:Accession: I50241; JC4618

R;Kaplan, M.H.; Smith, D.I.; Sundick, R.S.  
J. Immunol. 151, 628-636, 1993  
A;Title: Identification of a G protein coupled receptor induced in activated T cells.  
A;Reference number: I50241; MUID:93329058; PMID:8393036  
A;Accession: I50241  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-308 <XAP>  
A;Cross-references: UNIPROT:P32250; UNIPARC:UPI0000055A6B; GB:L06109; NID:G304383; PIDN:  
R;Webb, T.E.; Kaplan, M.G.; Barnard, E.A.  
Biochem. Biophys. Res. Commun. 219, 105-110, 1996  
A;Title: Identification of 6H1 as a P2Y purinoceptor: P2Y5.  
A;Reference number: JC4618; MUID:96190677; PMID:8619790  
A;Accession: JC4618  
A;Molecule type: mRNA  
A;Residues: 1-308 <WEB>  
A;Cross-references: UNIPARC:UPI000055A6B; GB:L06109; NID:G304383; PIDN:AAB06587.1; PID:  
A;Experimental source: T-cells  
C;Comment: This receptor plays a role in T-cell activation.  
C;Genetics:  
A;Gene: p2y5  
C;Superfamily: ATP receptor P2u  
C;Keywords: G protein-coupled receptor; transmembrane protein  
P;15-40/Domain: transmembrane #status predicted <TM1>  
P;51-74/Domain: transmembrane #status predicted <TM2>  
P;89-109/Domain: transmembrane #status predicted <TM3>  
P;133-153/Domain: transmembrane #status predicted <TM4>  
P;177-201/Domain: transmembrane #status predicted <TM5>  
P;227-248/Domain: transmembrane #status predicted <TM6>  
P;269-292/Domain: transmembrane #status predicted <TM7>

Query Match 22.8%; Score 368.5; DB 2; Length 308;  
Best Local Similarity 30.3%; Pred. No. 1.6e-26;  
Matches 91; Conservative 64; Mismatches 102; Indels 43; Gaps 10;  
Matches 91; Conservative 64; Mismatches 102; Indels 43; Gaps 10;

QY 10 SSDDLTPWPAIKLGFYAYLGVLLVGLLNSLALWVFCRMOQWETRIYMTNLAVADLC 68  
Db 3 SSSCSTEDSKYLYGCVFWSVFLGLNLCVAVIIFTLKVRNETTYMLMLAISDLL 62

QY 69 LLCTLPFVLHSLRDTSDTP----LCQLSQGIYLTNRYSISLVTIAVDYVAVRHPLRA 124  
Db 63 FVFTLPFRIFYF-VVRNWPFGDLCKISVTLFTYNNYGSILPLTCSVDRFLAIVHPFS 121

QY 125 RGLRSPROAAVCAVLWLVVI-GSLVARMLLGIQEGGFCRST-RUNFNSMR-----FP- 176  
Db 122 KTLRTKRNARIVCAVMTVLASTPSF-----FQSTNRQNTEQRTCFENFPE 171

QY 177 -----LLGFYPLAVVFCSLKVVVTAQAORPPTDVQAEATRAARMVWA 221  
Db 172 STWKTYLSRIVPIEIVGFPIILNVTCTMVLRTL-NKPLTSLRNKLSKKVLMKIFV 230

QY 222 NLVVFVVCFLPHVGL---TVRLAVGNACALLTERRALYITSKLSDANCCLDAICY 278  
Db 231 HLIVFCFCFVPYNTILILSLMETQWINGSVVTARTWYPTVLCAVSNCCFDPVIVYF 290

RESULT 3  
I69202  
G protein-coupled receptor HM74 - human  
C;Species: Homo sapiens (man)  
C;Date: 12-Aug-1996 #sequence\_revision 12-Aug-1996 #text\_change 09-Jul-2004  
C;Accession: I69202  
R;Nomura, H.; Nielsen, B.W.; Matsushima, K.  
Int. Immunol. 5, 1239-1249, 1993  
A;Title: Molecular cloning of cDNAs encoding a LD78 receptor and putative leukocyte chem  
A;Reference number: I54751; MUID:94092629; PMID:7505609  
A;Accession: I69202  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-387 <RES>  
A;Cross-references: UNIPROT:P49019; UNIPARC:UPI0000043C3C; GB:D10923; NID:G219866; PIDN:  
C;Genetics:  
A;Gene: HM74

C;Superfamily: G protein-coupled receptor 4  
Query Match 22.8%; Score 368.5; DB 2; Length 387;  
Best Local Similarity 34.3%; Pred. No. 2.1e-26;  
Matches 95; Conservative 48; Mismatches 105; Indels 29; Gaps 11;

QY 27 LGVLVGLLNSLALWVFCRMOQWETRIYMTNLAVADLCCLCTLPVL-----HSLR 81  
Db 34 LGLEPIFGLLNGLALWVFCRMOQWETRIYMTNLAVADLCCLCTLPVL-----HSLR 93

QY 82 DTSDFPLCQLSQGIYLTNRYSISLVTIAVDYVAVRHPLRAARGLRSPROAAVCAVLW 141  
Db 94 NFGDIP-CELVLFEMAMRQSGIIFLTVAVDYVAVRHPLRAARGLRSPROAAVCAVLW 152

QY 142 VLVIQ---SLVARMLLGIQEG--GFCFR-STRHNF--NSMRPPLGLFYPLAVVFCSLK 193  
Db 153 GITVGLTVHLLKKLL-LQGNPANVCISFISICTERWEAMF-LLEFLPLGLIILFCSAR 210

QY 194 VVTAQAORPPTDVQAEATRAARMVWNLVFCFLPHVGLTVRLAVGW-----N 246  
Db 211 IISLRQ---QMDRHAKIKRAITFIMVAVIVFICPLP---SVVVRIRIFMLHTSGTQ 264

QY 247 ACALLETRRALLYITSKLSDANCCLDAICYVMKEF 283  
Db 265 NCEVRSVDLAPFILTSTYNNSMMLDPVYVFPSSPSP 301

RESULT 4  
T09508  
Intron 17 purinergic receptor P2Y5 - human  
N;Alternate names: G-protein coupled receptor  
C;Species: Homo sapiens (man)  
C;Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 09-Jul-2004  
C;Accession: T09508  
R;Bohm, S.K.; Trummel, A.; Khitin, L.M.; Kong, W.; Payan, D.G.; Bunnett, N.W.  
submitted to the EMBL Data Library, April 1997  
A;Description: The human purinergic receptor P2Y5 is encoded in intron 17 of the retinob  
A;Reference number: Z16705  
A;Accession: T09508  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-344 <BOH>  
A;Cross-references: UNIPROT:P43657; UNIPARC:UPI000005041B; EMBL:AF000546; NID:G2232068; I  
C;Genetics:  
A;Map position: 13  
C;Superfamily: ATP receptor P2u  
C;Keywords: G protein-coupled receptor; transmembrane protein

Query Match 22.3%; Score 360.5; DB 2; Length 344;  
Best Local Similarity 29.2%; Pred. No. 1e-25;  
Matches 90; Conservative 68; Mismatches 107; Indels 43; Gaps 10;

QY 10 SSDDLTPWPAIKLGFYAYLGVLLVGLLNSLALWVFCRMOQWETRIYMTNLAVADLC 68  
Db 6 SHCFYNSFKYLYGCMFWSVFLGLVSNCAIYIFICLVKVRNETTYMLNLSDDL 65

QY 69 LLCTLPFVLHSLRDTSDTP----LCQLSQGIYLTNRYSISLVTIAVDYVAVRHPLRA 124  
Db 66 FVFTLPFRIFYF-TTRNWPFGDLCKISVMLPYTNNYGSILPLTCSVDRFLAIVVFPKS 124

QY 125 RGLRSPROAAVCAVLWLVVI-GSLVARMLLGIQEGG-----FCFRSTRHNFNSMRFP-- 176  
Db 125 KTLRTKRNARIVCTGVMTLVIGGSAPAVFVOSTHSGQNNASEACPEN-----FPEA 175

QY 177 -----LLGFYPLAVVFCSLKVVVTAQAORPPTDVQAEATR-KAARMVWA 221  
Db 176 TWKTYLSRIVPIEIVGFPIILNVTCTSSWVLKTLTK--PVTLRSKINKTKVLMKIFV 233

QY 222 NLVVFVVCFLPHVGLTVRLAVGNWNA---CALLETIRRALYITSKLSDANCCLDAICY 278  
Db 234 HLIVFCFCFVPYNTILILYSLVTRTQTFVNCVSWAAVRTWYPTVLCAVSNCCFDPVIVYF 293

QY 279 MAKEFQEA 286

Db 294 TSDTIQNS 301

RESULT 5  
155450

G protein-coupled P2 receptor - rat  
C:Species: Rattus norvegicus (Norway rat)  
C>Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 09-Jul-2004  
C:Accession: I55450  
R:Chang, K.; Hanaoka, K.; Kumada, M.; Takuwa, Y.  
J. Biol. Chem. 270, 26152-26158, 1995  
A:Title: Molecular cloning and functional analysis of a novel P2 nucleotide receptor.  
A:Reference number: I55450; MUID:96064682; PMID:7592819  
A:Accession: I55450  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-328 <RES>  
A:Cross-references: UNIPROT:Q63371; UNIPARC:UPI0000131003; GB:D63665; NID:g1066007; PIDN:  
C:Superfamily: ATP receptor P2u  
C:Keywords: G protein-coupled receptor

Query Match 19.8%; Score 319; DB 2; Length 328;  
Best Local Similarity 30.6%; Pred. No. 6.6e-22;  
Matches 96; Conservative 48; Mismatches 130; Indels 40; Gaps 11;

QY 2 NGTY-----NTCGSSD-----LTWPPAIKLGFYAVLGVLLVGLLNSLALWVFCRMQ 50  
DB 5 NGTIQAGLPPTTCVYREDFKRLPPV-----YSVVLVGLPLNVCVIAQICASRR 56  
QY 51 QWTEIRYMTNLAVADLCCLCTLPFVLHSLRDTSDTLP-----COLSQGIYLTNRYSISL 106  
DB 57 TTRSAVYTLNLAADLLYACSLPIIYNYARGDHPFGDLACRLVFLFYANLHGSILP 116  
QY 107 VTAIAVDYVAVRHPLRGLRSPQAA-AVCALVWLVLVIGSLVARWLL---GIQEG-GF 161  
DB 117 LTCISFQYLGICHPLAPWHKGGREAAWVGVWLVTVAQCLPTAVFAATGIQRNRTV 176  
QY 162 CP-----RSTRHNFSMRPPLGLFVLAVVVFCSLKVVTALAQR--PPTDVGQAEATR 213  
DB 177 CYDLSPPILSTRYLPYGMALTIVIGFLPPTALLACYCRMARLRCQDGPAGVQAQ-ERRS 235  
QY 214 KAARVMWANLVVVCFLPLHGLTVRLAVGWN---ACALLETIRRALYITSKLSANCC 270  
DB 236 KAARMAVVAAPVLSFLPHTKTYLAVRTPGVSCPVLETFAAAYKTRPPASNSV 295  
QY 271 LDAICYNNMAKBFQ 284  
DB 296 LQPLFYFQQKFR 309

RESULT 6  
ATP receptor P2u - mouse  
C:Species: Mus musculus (house mouse)  
C>Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 09-Jul-2004  
C:Accession: A47556  
R:Lustig, K.D.; Shiau, A.K.; Brake, A.J.; Julius, D.  
Proc. Natl. Acad. Sci. U.S.A. 90, 5113-5117, 1993  
A:Title: Expression cloning of an ATP receptor from mouse neuroblastoma cells.  
A:Reference number: A47556; MUID:93281707; PMID:7685114  
A:Accession: A47556  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-373 <LUS>  
A:Cross-references: UNIPROT:P35383; UNIPARC:UPI0000027DFV; GB:L14751; NID:g309457; PIDN:  
C:Superfamily: ATP receptor P2u  
C:Keywords: transmembrane protein

Query Match 19.8%; Score 319; DB 2; Length 373;  
Best Local Similarity 30.1%; Pred. No. 7.5e-22;  
Matches 101; Conservative 54; Mismatches 130; Indels 50; Gaps 11;

QY 2 NGTYNTCGSSDLTWPPAIKLG-----YAYL-----GVLLVGLLNSLALWVFCR 48  
DB 9 NSTINGTWEGD-----ELGKCRFNEDFKYVLLPVSYGVVCLGLCLNVVALYIFLR 61  
QY 49 MQOWTEIRYMTNLAVADLCCLCTLPFVLHSLRDTSDTP-----LCQLSQGIYLTNRYSI 104  
DB 62 LKTNASTYTMPHLAVSDLSYAASLFLVLYYARGDHPFPSTVLCVLRFLFYTLNLYCSI 121  
QY 105 SLVTAIAVDYVAVRHPLRGLRSPQAAAVCAVLVWLVLVIGSLVARWLLGIQEGGFCFR 164  
DB 122 LFLTCISVHRCLGVLPFLHSLRWGFRVARRVAAVWVLVL-ACQAPVLYFVTTSVRGTR 180  
QY 165 STRHN-----PNSMRFPPLGLFVLAVVVFCSLKVVTALAQRPP--TDVGQAE 210  
DB 181 ITCHDTSARELFSHFVAYSSVMGLL-FAVPFSVLVGVLMARLL-KPAYGTGGGLPR 238  
QY 211 ATRKAARMWANLVVVCFLPLHGLTVRLAVGWN---NACALLETIRRALYITSKLSAN 268  
DB 239 AKRSVRTIALVLAVALCFLPFHVTRTYYSFRSLDUSCHTLNAINWYKTRPLASAN 298  
QY 269 CCLDAICYNY-----MAKEFOEASALAVAPRAK 296  
DB 299 SCLDPVLYLAGQRLVRFARDAKPTEPTSPQAR 333

RESULT 7  
S33733  
G protein-coupled receptor - chicken  
C:Species: Gallus gallus (chicken)  
C>Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 09-Jul-2004  
C:Accession: S33733  
R:Webb, T.E.; Simon, J.; Kriehak, B.J.; Bateson, A.N.; Smart, T.G.; King, B.F.; Burnstock  
FEBS Lett. 324, 219-225, 1993  
A:Title: Cloning and functional expression of a brain G-protein-coupled ATP receptor.  
A:Reference number: S33733; MUID:93285340; PMID:8508924  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-362 <WEB>  
A:Cross-references: UNIPROT:P34996; UNIPARC:UPI00000405D4; EMBL:X73268; NID:g395084; PTI:  
C:Superfamily: ATP receptor P2u  
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 19.7%; Score 318; DB 2; Length 362;  
Best Local Similarity 28.2%; Pred. No. 9e-22;  
Matches 96; Conservative 63; Mismatches 134; Indels 48; Gaps 12;

QY 1 MNGTY-----NTCGSSDLTWPPAIKLG-YAYLGVLLVL---GLLNSLALWV 44  
DB 10 LNGTQPELLAGGAAAGNATTKCSLT-----KTGFQFYLPTVVILVITGFLGNSVAIWM 64  
QY 45 FCRMQOWTEIRYMTNLAVADLCCLCTLPFVLHSLRDTSD-----TPLCQLSQGIYLTNR 100  
DB 65 FVFHMRPWSGISVYTMFLALADFLVYLTLPALIFYFNKTDWIFGDMCKLQRFIFHVL 124  
QY 101 YMSISIVTAIAVDYVAVRHPLRGLRSPQAAAVCAVLVWLVLVIGSLVARWLL---GI 156  
DB 125 YGSIILFLTCISVHRVTGVVHPLKSLGRKKNAVYSSLVWLVV-AVIAPILFYSGTGV 183  
QY 157 QBGQ--FCFRSTRHN-----NSMRFPPLGLFVLAVVVFCSLKVVTALAQRPPDVQG 208  
DB 184 RENKTICTDITADEYLSYFVYVSMCTTVMFCIPFVLGCVGLIVKALIVK---DLDN 240  
QY 209 AEATRKAAARMWANLVVVCFLPLHGLTVRLAVGWN-----ACALLETIRRALYITSK 263  
DB 241 SPLRRKSIYLVITVFAVSYLPFHVMTKLNLRALDFQTPQMCAFNQDKVYATYQVTRG 300  
QY 264 LSDANCCLDACYNNMAKEFOEASALAVAPRAKAKHSQDSL 304  
DB 301 LASLNSCVDPILYLAGDTFR--RLSRATRKSSRRSEPNV 339

RESULT 8

S68679

G protein-coupled receptor - human  
C/Species: Homo sapiens (man)  
C/Date: 15-Feb-1997 #sequence\_revision 13-Mar-1997 #text\_change 09-Jul-2004  
C/Accession: S68679  
R/Stam: N.J.; Klomp, J.; van de Heuvel, M.; Olijve, W.  
FEBS Lett. 384, 260-264, 1996  
A/Title: Molecular cloning and characterization of a novel orphan receptor (P2P) expressed in the rat brain  
A/Reference number: S68679; MUID:96197801; PMID:8617367  
A/Accession: S68679  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-365 <STA>  
A/Cross-references: UNIPROT:P51582; UNIPARC:UPI000002E776; EMBL:X65597; NID:gl296631; PID:gl296631  
C/Suprafamily: ATP receptor P2u  
C/Keywords: G protein-coupled receptor

Query Match 19.58; Score 315.5; DB 2; Length 365;  
Best Local Similarity 29.18; Pred. No. 1.5e-21;  
Matches 93; Conservative 55; Mismatches 127; Indels 45; Gaps 11;  
Qy 29 VLVVLGLLNSLALVPCCRMQQWETRIYMTNLAVADLCLCTLPFLVLSLSDTSDTP- 87  
Db 44 VVFLVGLGLNAPTLMLFIFELRPWDATATYMFHLASDITLVLSPLTIYYAAHNPWF 103  
Qy 88 ---LCQLSQGIYITNRYMSISLVTATADVAVRHPRLARGURSPQAAAVCAVLVVLV 144  
Db 104 GTBICKVRFVFLWNLVCSVLFITCISVHYLGICHPRLARGURPRLAGLLCLAVMLVV 163  
Qy 145 IGSIVAR-WLLGQEGQ---PCPRSTR-----H--NFNSMRPFLGLPPLAVVVCSLK 193  
Db 164 AGCLVPLNLFVTTNSKGTTLVCHDTTRPEFDHYVFPSSAVMGLL-FGVPLVTLVCYGL 222  
Qy 194 VVTALARPPTDVGQARATKAARVMWANLVVFCFLPLHVLGTV----RLAVGNWACA 249  
Db 223 MARLYQ-PLPGSNQSSRLRSLEITIAVLTVFVAVCFPHITITTYLARLLEA--DCR 279  
Qy 250 LLETIRBALYITSKLSDANCLDAICYVMKAFQEQ-----ASALAVAP 293  
Db 280 VLVNIVNYYKTRPLASANSCLDPVLYLLTGDKYRQLRQLCGGKQPQRTAASSLALVS 339  
Qy 294 RAK-----AHKSQDSLCVT 307  
Db 340 LPEDSSCRWAATPQDSSCST 359

RESULT 9

QJ1488  
bradykinin B2 receptor - human  
C/Species: Homo sapiens (man)  
C/Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 09-Jul-2004  
C/Accession: JH0712; A46022; A55559; JQ1488; JCI1400  
R/Eggerickx, D.; Raspe, E.; Bertrand, D.; Vassart, G.; Parmentier, M.  
Biochem. Biophys. Res. Commun. 187, 1306-1313, 1992  
A/Title: Molecular cloning, functional expression and pharmacological characterization of the human bradykinin B2 receptor  
A/Reference number: JH0712; MUID:93039601; PMID:1329734  
A/Accession: JH0712  
A/Molecule type: DNA  
A/Residues: 1-364 <EGG>  
A/Cross-references: UNIPROT:P30411; UNIPARC:UPI000002A4FC; GB:S45489; NID:g2565336; PIDN:R/Powell, S.J.; Slyn, G.; Thomas, C.; Hopkins, B.; Briggs, I.; Graham, A.  
Genomics 15, 435-438, 1993  
A/Title: Human bradykinin B2 receptor: nucleotide sequence analysis and assignment to chromosome 15  
A/Reference number: A46022; MUID:93194199; PMID:7916737  
A/Accession: A46022  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-364 <POM>  
A/Cross-references: UNIPARC:UPI000002A4FC; GB:S56772; NID:g298604; PIDN:AAB25765.1; PID:gl298604  
A/Note: sequence extracted from NCBI backbone (NCBIN:127280, NCBI:P127284)  
R/Ma, J.; Wang, D.; Ward, D.C.; Chen, L.; Deesai, T.; Chao, J.; Chao, L.  
Genomics 23, 362-369, 1994  
A/Title: Structure and chromosomal localization of the gene (BDKRB2) encoding human bradykinin receptor type B-2 - rat

A/Reference number: A55559; MUID:95137582; PMID:7835885

A/Accession: A55559  
A/Molecule type: DNA  
A/Residues: 1-364 <MAA>  
A/Cross-references: UNIPARC:UPI000002A4FC; GB:L27594  
R/Hess, J.F.; Borkowski, J.A.; Young, G.S.; Strader, C.D.; Ransom, R.W.  
Biochem. Biophys. Res. Commun. 184, 260-268, 1992  
A/Title: Cloning and pharmacological characterization of a human bradykinin (BK-2) receptor  
A/Reference number: JQ1488; MUID:92231936; PMID:1314587  
A/Accession: JQ1488  
A/Molecule type: mRNA  
A/Residues: 1-364 <HES>  
A/Cross-references: UNIPARC:UPI000002A4FC; GB:M88714; NID:gl387999; PIDN:AAB02793.1; PID:gl387999  
C/Genetics: GDB:BDKRB2  
A/Gene: GDB:BDKRB2  
A/Cross-references: GDB:135713; OMIM:113503  
A/Map position: 14q32.1-14q32.2  
A/Introns: #status absent  
A/Suprafamily: vertebrate rhodopsin  
C/Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane protein; F;34-56/Domain: transmembrane #status predicted <TM1>  
F;66-92/Domain: transmembrane #status predicted <TM2>  
F;104-127/Domain: transmembrane #status predicted <TM3>  
F;148-171/Domain: transmembrane #status predicted <TM4>  
F;195-221/Domain: transmembrane #status predicted <TM5>  
F;241-266/Domain: transmembrane #status predicted <TM6>  
F;285-309/Domain: transmembrane #status predicted <TM7>  
F;312,180/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F;242/Binding site: phosphate (Thr) (covalent) (by protein kinase A) #status predicted  
F;316/Binding site: phosphate (Ser) (covalent) (by protein kinase A) #status predicted  
Query Match 19.44; Score 312.5; DB 2; Length 364;  
Best Local Similarity 27.64; Pred. No. 2.9e-21;  
Matches 89; Conservative 54; Mismatches 128; Indels 51; Gaps 9;  
Qy 1 MNGTYNTCGSSDLTW-----PPAIIKGLGFAYIGLVLLVGLLNSLALVPCCRMQW 52  
Db 11 LMGTFQAQSKCPQVWGLWGLNTIQQP-----FLWVLEVLATLENIFVLVSFLCHKSSC 62  
Qy 53 TETRIYMTNLAVADLCLCTLPFLVLSLSDTSD---TPLCQLSQGIYITNRYMSISLVT 108  
Db 63 TVAEIYGLNLAADLILACGLFPWALTISNNFNDLPGFETLCRWVNAIISNLYSSICFLM 122  
Qy 109 ATADVAVRHPRLARGURSPQAAAVCAVLW--VLVIGS--LVARWLLGQEGGFCFR 164  
Db 123 LVSIDRYLALVKTSMGRNMGVRWAKLYSLVWGTCTLLSSPMLVPTMKYSDEG---- 178  
Qy 165 STRHN-----FNSMRPPLAGVYLPLAVVVCSLKVVVTLAQRPPPTDVGOA 209  
Db 179 ---HNVTAQVSYPSLIWVFTNMLNIVVGLPLPSVITFTMQIMQVLRNEMQKPKFI 235  
Qy 210 EATKKAARVMWANLVVVCFLPLHVLGTV----RLAVGNWACALLETIRRALYITSKLS 265  
Db 236 QTERRATVLVVLVLLFIICWLPFQISTPLDTLRLGI--LSSQDERIIDVITQIASFMA 294  
Qy 266 DANCLDAICYVMKAFQEQAS 287  
Db 295 YSNSCLNPLVYVIVGKRFKKS 316  
RESULT 10  
CORTB2  
bradykinin receptor type B-2 - rat  
C/Species: Rattus norvegicus (Norway rat)  
C/Date: 30-Sep-1992 #sequence\_revision 30-Sep-1992 #text\_change 09-Jul-2004  
C/Accession: A41283; A55079; S47529  
R/McSachern, A.E.; Shelton, E.R.; Bhakta, S.; Obermole, R.; Bach, C.; Zuppan, P.; Fujise  
Proc. Natl. Acad. Sci. U.S.A. 88, 7724-7728, 1991  
A/Title: Expression cloning of a rat B-2 bradykinin receptor.  
A/Reference number: A41283; MUID:91352062; PMID:1715575  
A/Accession: A41283  
A/Molecule type: mRNA

A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-342 <HON>  
A:CROSS-references: UNIPROT:P01556; UNIPARC:UPI00001311EE; GB:X56736; NID:G94442; PIDN:  
A>Note: the species of guinea pig is not identified; in GenBank entry CCAPAFREC, release  
C:Superfamily: ATP receptor P2U

Query Match 19.2%; Score 310; DB 2; Length 342;  
Best Local Similarity 28.2%; Pred. No. 4.7e-21;  
Matches 81; Conservative 58; Mismatches 110; Indels 38; Gaps 9;

Qy 29 VLVVLGLLLNSLALWVFCRM---QQWTETRIYMTNLAVADLCCLCTLP--FVLHSURDT 83  
Db : : ||| : ||| :  
24 IIFVLGIANGVYLWVF-ARLYPSKLNKEIKFMVNLTVDALLFLITPLWLVIYYSQGN 82  
Qy 84 SDTP--LCQLSQIGIYLTNRWYMSISLVTAIAVDRYVAVRHPLRARGLSRPQAACVAVLW 141  
Db :  
83 WFLPKFLCNAGCLFFINTYCSVAFLGVIYTNRFQAVKYPIKTAQATRKRGIALSLVIW 142  
Qy 142 VLVTGSIVARWLGIQIB-----GGCFSTRHNFNFSMRPPL-----LGFYILPLA 185  
Db :  
143 VAIVA--ASYFLVMDSNTNVSNKAGSNTRCFEHYEKGSKPVLIITHICVLGFFIVFL 200  
Qy 186 VWVFCSLKVVTALAQRPTDVGQAEATRKAARMVMWANLLVFVVCFLPLHVGLTVRLAVGW 245  
Db : : ||| :  
201 LILFCNLVIIHTLRQVPKQORNAEVERRALWMVCTVLAVFVICFPVPHM-----VOLPW 255  
Qy 246 NCACL-----LETIRRAYITSKSGDANCCLDALCIYYMAKEPOE 285  
Db :  
256 TLAEIGMPSSNHQAINDAHQVTLCLLSTNCVLDPFVICYELTKKKFRK 302

RESULT 12  
A54946  
P-2U nucleotide receptor - human  
C:Species: Homo sapiens (man)  
C>Date: 11-Nov-1994 #sequence\_revision 11-Nov-1994 #text\_change 17-Mar-1999  
C:Accession: A54946  
R:Parrr, C.E.; Sullivan, D.M.; Paradiso, A.M.; Lazarowski, E.R.; Burch, L.H.; Olsen, J.C.  
Proc. Natl. Acad. Sci. U.S.A. 91, 3275-3279, 1994  
A>Title: Cloning and expression of a human P-2U nucleotide receptor, a target for cystinosis  
A:Reference number: A54946; MUID:94211846; PMID:8159738  
A:Accession: A54946  
A>Status: preliminary  
A:Molecule type: mRNA; protein  
A:Residues: 1-375 <PAR>  
A:CROSS-references: UNIPARC:UPI0000145104; GB:U07225  
A>Note: parts of this sequence were confirmed by protein sequencing  
C:Genetic8;  
A:Gene: GDB:P2RY2; HP2U; P2U  
A:CROSS-references: GDB:362713; OMIM:600041  
A:Map position: 11q13.5-11q14.1  
C:Superfamily: ATP receptor P2U  
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 19.1%; Score 308.5; DB 2; Length 375;  
Best Local Similarity 31.7%; Pred. No. 7.1e-21;  
Matches 89; Conservative 41; Mismatches 104; Indels 47; Gaps 8;

Qy 28 GVVLVLGLLLNSLALWVFCRMQQWTETRIYMTNLAVADLCCLCTLPFVLSLRDSTDTP 87  
Db : : ||| : ||| :  
41 GWCVVLGCLNAVGLIYPLCKLKTNASTTTTFHLAVSDALYAASFLPLVVYYARGDHP 100  
Qy 88 ----LCQLSQIGIYLTNRWYMSISLVTAIAVDRYVAVRHPLRARGLSRPQAACVAVLW 143  
Db :  
101 FSTVLCKLVRFLFYTNLYCSILFTLCISHRHCLGVLRPLRSRWGRARYARRVAGAVWL 160  
Qy 144 VTGSIVARWLGIQIBGGCFSTRHNFNFSMRPPL-----LGF 180  
Db 161 V-----LACQAPVLYFVTT-----SARGPLTCHDTSAPELSFREYAYSSVMGLLF 206  
Qy 181 YLPLAVVWFCSLKVTALAQRP--TDVGOEAETKAAARMWVANLLVFVVCFLPLHVLGT 238  
Db : : ||| :  
Qy : : ||| :

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Db      207 AVFFAVILVCYVLMARRLL-KPAYTSGGLPRAKRKSVRTIAVVLAVFALCFLPFHVTRT 265
QY      239 VRLAVGW--NACALLTIRRALYITSKLSDANCLDAICY 277
Db      266 LYTSPRSLDLSCHTLNAINNA-YKVTRLASANCLDPVLYF 305

RESULT 13
IS3033
G protein-coupled receptor - human
C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
R;Heiber, M.; Docherty, J.M.; Shah, G.; Nguyen, T.; Cheng, R.; Heng, H.H.Q.; Marchese, A
DNA Cell Biol. 14, 25-35, 1995
A;Title: Isolation of three novel human genes encoding G protein-coupled receptors.
A;Reference number: IS3033; MUID:95134353; PMID:7832990
A;Accession: IS3033
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-354 <RES>
A;Cross-references: UNIPROT:P46093; UNIPARC:UPI0000016A9DF; GB:L36148; NID:g598152; PIDN:
C;Superfamily: G protein-coupled receptor 4
C;Keywords: G protein-coupled receptor

Query Match      18.9%; Score 305.5; DB 2; Length 354;
Best Local Similarity 31.0%; Pred. No. 1.3e-20;
Matches 93; Conservative 48; Mismatches 118; Indels 41; Gaps 11;

QY      2 NGTYNTC---GSSDLTWPPAIIKGFVAYILGVLLVGLLNSLALWVFCRMOQWTETRIY 58
Db      3 NHTWEGCHVDSRVDHLFPFSL-----YIFVIGV-GLPTNCLALWAAVYQVQRNQLGY 55

QY      59 MTNLAVADLCLLCTLP-----FVLHSLRDTSDTLPCLSQGIYLTNRYSISLVTAIAVDR 114
Db      56 LNNLSIADLLYICTLPVWDVDFLHNDNWIHGPSCKLGFGFVFNIVYISIAFLCCISVDR 115

QY      115 YVAVRHPLRARGLRSPQAAACAVLWLVIGSLVARWLLGIOEGGFCFRST-RHNFSM 173
Db      116 YLAVAHPLRFLRRVKTAVAVSSVWATLGGANSAP--LFHDE---LFRDRYNTHTFCPE 170

QY      174 RPPL-----LGFYLPVAVVFCSLKVVTALAQRPPTDVGOAEATRKAAVMW 220
Db      171 KFPMEGWAMNLYRVFVGLFPWMLLSYRGILRAVGSVST---ERQEKAKIKRLAL 227

QY      221 ANLLVFWVCFPLHVLGLTVRLAV-----GWNACALLETIRRALYITSKLSDANCLDAICY 276
Db      228 SLIAIIVLCFAPYHVLLLSRSAILVGRPWD-CGFEERVFSAYHSSLAFTSLNCVADPILY 286

QY      174 RPPL-----LGFYLPVAVVFCSLKVVTALAQRPPTDVGOAEATRKAAVMW 220
Db      171 KFPMEGWAMNLYRVFVGLFPWMLLSYRGILRAVGSVST---ERQEKAKIKRLAL 227

QY      221 ANLLVFWVCFPLHVLGLTVRLAV-----GWNACALLETIRRALYITSKLSDANCLDAICY 276
Db      228 SLIAIIVLCFAPYHVLLLSRSAILVGRPWD-CGFEERVFSAYHSSLAFTSLNCVADPILY 286

RESULT 14
A57641
G protein-coupled receptor 4 - human
C;Species: Homo sapiens (man)
C;Date: 08-Feb-1996 #sequence_revision 08-Feb-1996 #text_change 09-Jul-2004
C;Accession: A57641
R;Mahadevan, M.S.; Baird, S.; Bailly, J.E.; Shutler, G.G.; Sabourin, L.A.; Tailfidi, C.
Genomics 30, 84-88, 1995
A;Title: Isolation of a novel G protein-coupled receptor (GPR4) localized to chromosome
A;Reference number: A57641; MUID:96129306; PMID:8595909
A;Accession: A57641
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-362 <NAH>
A;Cross-references: UNIPROT:P46093; UNIPARC:UPI0000050428; GB:U21051; NID:g687793; PIDN:
C;Genetics:
A;Gene: GPR4
A;Cross-references: GDB:371710; OMIM:600551
A;Map position: 19q13.3-19q13.3
A;Introns: #status absent
C;Superfamily: G protein-coupled receptor 4
C;Keywords: G protein-coupled receptor
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Query Match      18.9%; Score 305.5; DB 2; Length 362;
Best Local Similarity 31.0%; Pred. No. 1.3e-20;
Matches 93; Conservative 48; Mismatches 118; Indels 41; Gaps 11;

QY      2 NGTYNTC---GSSDLTWPPAIIKGFVAYILGVLLVGLLNSLALWVFCRMOQWTETRIY 58
Db      3 NHTWEGCHVDSRVDHLFPFSL-----YIFVIGV-GLPTNCLALWAAVYQVQRNQLGY 55

QY      59 MTNLAVADLCLLCTLP-----FVLHSLRDTSDTLPCLSQGIYLTNRYSISLVTAIAVDR 114
Db      56 LNNLSIADLLYICTLPVWDVDFLHNDNWIHGPSCKLGFGFVFNIVYISIAFLCCISVDR 115

QY      115 YVAVRHPLRARGLRSPQAAACAVLWLVIGSLVARWLLGIOEGGFCFRST-RHNFSM 173
Db      116 YLAVAHPLRFLRRVKTAVAVSSVWATLGGANSAP--LFHDE---LFRDRYNTHTFCPE 170

QY      174 RPPL-----LGFYLPVAVVFCSLKVVTALAQRPPTDVGOAEATRKAAVMW 220
Db      171 KFPMEGWAMNLYRVFVGLFPWMLLSYRGILRAVGSVST---ERQEKAKIKRLAL 227

QY      221 ANLLVFWVCFPLHVLGLTVRLAV-----GWNACALLETIRRALYITSKLSDANCLDAICY 276
Db      228 SLIAIIVLCFAPYHVLLLSRSAILVGRPWD-CGFEERVFSAYHSSLAFTSLNCVADPILY 286

RESULT 15
S60024
bradykinin B1 receptor - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 24-Aug-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
A;Accession: S60024
R;MacNeill, T.; Bieri, K.K.; Menke, J.G.; Hees, J.F.
Biochim. Biophys. Acta 1264, 223-228, 1995
A;Title: Cloning and pharmacological characterization of a rabbit bradykinin B(1) recept
A;Reference number: S60024; MUID:96085127; PMID:7495867
A;Accession: S60024
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-352 <MAC>
A;Cross-references: UNIPROT:P48748; UNIPARC:UPI0000126ABF; EMBL:U20507; NID:g1041820; PI
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; transmembrane protein

Query Match      18.9%; Score 305; DB 2; Length 352;
Best Local Similarity 26.6%; Pred. No. 1.4e-20;
Matches 89; Conservative 62; Mismatches 131; Indels 52; Gaps 10;

QY      7 TCGSSDLTWPPAIIKGFVAYILGVLLVGLLNSLALWVFCRMOQWTETRIYMTNLAVAD 66
Db      24 SCGAPDADWDLHRL-LPTFIITITLGLLNSFVLSVFLARRLSVAEIVLANLAASD 82

QY      67 LCLLCTLPFVLHSLRDTSDTP-----LCQLSQGIYLTNRYSISLVTAIAVDRYAVRHPL 122
Db      83 LVFVLGLPFAENVRNQDPWPGALCRVINGVIKANLFISIFLVVAISQDRYSVLVHDM 142

QY      123 RARGLRSPQAAACAVLWLVIGSLVARWLLGIOEGGFCFRSTR-----167
Db      143 ASRRGRRRQAQCALIW--LAGGL-----LSTPTFVLSRAVPELVNASACILLP 193

QY      168 -----HNFNSMRPFLGFLYPLAVVVFCSLVKVTAL---AQRPPTDVGOAEATRKAAVMW 220
Db      194 HEAWHLRMVELNLGLFLPLAAILFNCIIILARRGERVPSRCGPRDSKSTA-LIL 252

QY      221 ANLLVFWVCFPLHVLGLTVRL-----AVGWNACALLETIRRALYITSKLSDANCLDAICY 275
Db      253 TLVASFLVCWAPYHFFAFLECLMQVHAIG--GCFWEEPTDLGLQLSNFSAFVNSCLNPVI 310

QY      276 YYMAKEP-----QEASALAVAPRAKAKSHQ 301
Db      311 YVFGRLFRKYVWELCQCQSPRSLAPVSSSRKE 344

Search completed: February 9, 2006, 01:01:14
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Mon Feb 13 13:14:00 2006

us-10-083-168-16.rpr

Page 7

Job time : 28.5 secs

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| Result No. | Query |       |        | DB ID   | Description        |
|------------|-------|-------|--------|---------|--------------------|
|            | Score | Match | Length |         |                    |
| 1          | 400   | 24.8  | 370    | JC5549  | heptahelical P2Y5- |
| 2          | 369.5 | 22.9  | 387    | I69202  | G protein-coupled  |
| 3          | 367.5 | 22.8  | 308    | I50241  | G protein-coupled  |
| 4          | 359.5 | 22.3  | 344    | T09508  | intron 17 purinerg |
| 5          | 317   | 19.6  | 373    | A47556  | ATP receptor P2u - |
| 6          | 316   | 19.6  | 362    | S33733  | G protein-coupled  |
| 7          | 315.5 | 19.5  | 365    | S68679  | G protein-coupled  |
| 8          | 314   | 19.4  | 328    | I55450  | G protein-coupled  |
| 9          | 311.5 | 19.3  | 354    | I53033  | G protein-coupled  |
| 10         | 311.5 | 19.3  | 362    | A57641  | G protein-coupled  |
| 11         | 311.5 | 19.3  | 364    | JQ1488  | bradykinin B2 rece |
| 12         | 311.5 | 19.3  | 366    | I0ORXB2 | bradykinin recepto |
| 13         | 309   | 19.1  | 342    | I13638  | platelet-activatin |
| 14         | 308.5 | 19.1  | 362    | B5741   | G protein-coupled  |
| 15         | 307.5 | 19.0  | 362    | S68207  | G protein-coupled  |
| 16         | 306.5 | 19.0  | 375    | A54946  | P-2U nucleotide re |
| 17         | 303   | 18.8  | 342    | A40191  | platelet-activatin |
| 18         | 303   | 18.8  | 352    | S60024  | bradykinin B1 rece |
| 19         | 300.5 | 18.6  | 373    | JC4162  | P2Y receptor - bov |
| 20         | 296.5 | 18.4  | 373    | JC4737  | G protein-coupled  |
| 21         | 292   | 18.1  | 341    | J43252  | platelet-activatin |
| 22         | 288   | 17.8  | 363    | JC2543  | angiotensin II rec |
| 23         | 286.5 | 17.7  | 352    | A43113  | chemokine (C-C) re |
| 24         | 286   | 17.7  | 328    | JC4800  | P2Y6 receptor - hu |
| 25         | 284.5 | 17.6  | 361    | B45880  | G protein-coupled  |
| 26         | 282   | 17.5  | 341    | S63666  | platelet activatin |
| 27         | 280.5 | 17.4  | 366    | I49519  | bradykinin B2 rece |
| 28         | 279.5 | 17.3  | 361    | JC5653  | G protein-coupled  |
| 29         | 278.5 | 17.2  | 363    | I57955  | somatostatin recep |

Int. Immunol. 5, 1239-1249, 1993  
A>Title: Molecular cloning of cDNAs encoding a LD78 receptor and putative leukocyte chemokine receptor  
A/Reference number: 154751; MUID:94092629; PMID:7505609  
A/Accession: 169202  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: mRNA  
A/Residues: 1-387 <RES>  
A/Cross-references: UNIPROT:P49019; UNIPARC:UPI0000043C3C; GB:D10923; NID:g219866; PIDN:169202  
C/Genetics:  
A/Gene: HW74  
C/Superfamily: G protein-coupled receptor 4

Query Match 22.9%; Score 369.5; DB 2; Length 387;  
Best Local Similarity 35.0%; Pred. No. 9.4e-27;  
Matches 98; Conservative 45; Mismatches 102; Indels 35; Gaps 12;

QY 27 LGVLLVGLGGLLSLALVFCRCMQWETRIYMTNLAVADLCCLCTLPVFL-----HSILR 81  
DB 34 LGLETFGLGLGLALWTFCHLKGWSSRIFFLENLAVADFLIICLPFVMDYVRRSDW 93

QY 82 DTSDFPLCOLSQGIYLTNRYMSISLTAIAVDYVAVRHPLRARGLRPRQAAAVCAVLW 141  
DB 94 NFGDIP-CRLVLFMFANRQGSIIFLTVAVDYFRVVPVHPHALNKISNWTAAIISCLLW 152

QY 142 VLVIG---SLVARWLLGIQEG--GFCFR--STRHNF--NSMRPPLGFLVPLAVVFCPSLK 193  
DB 153 GITVGLTVHLLKKLL-IONGANVCISFISCHTFRWHEAMF-LLEFLLPLGIIILFCSAR 210

QY 194 VVTALAQRPPTDVGAETRAKAKR---MVANLLVFCFLPLHVLGLTVRLAVGW----- 245  
DB 211 LIWSLRQ-----QMDRHAKIKRAITFIMVAIVFVICFLP---SVVVRIRIFLLHTS 261

QY 246 --NACALLETTIRALYITSKLSDANCLDAICYMAKEF 283  
DB 262 GTQNCVYRSVDLAFITLFTSYMSMLDPVVVYFSSPSF 301

RESULT 3  
150241  
A>Title: Identification of a G protein coupled receptor induced in activated T cells.  
A/Reference number: 150241; MUID:93329058; PMID:8393036  
A/Accession: 150241  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: mRNA  
A/Residues: 1-308 <KAP>  
A/Cross-references: UNIPROT:P32250; UNIPARC:UPI0000055A6B; GB:L06109; NID:g304383; PIDN:150241  
R/Weber, T.E.; Kaplan, M.G.; Barnard, E.A.  
Biochem. Biophys. Res. Commun. 219, 105-110, 1996  
A>Title: Identification of 6H1 as a P2Y purinoceptor: P2Y5.  
A/Reference number: JC4618; MUID:96190677; PMID:8619790  
A/Accession: JC4618  
A/Molecule type: mRNA  
A/Residues: 1-308 <WEB>  
A/Cross-references: UNIPARC:UPI0000055A6B; GB:L06109; NID:g304383; PIDN:AAB065897.1; PID:150241  
A/Experimental source: T-cells  
C/Comment: This receptor plays a role in T-cell activation.  
C/Genetics:  
A/Gene: p2Y5  
C/Superfamily: ATP receptor P2u  
C/Keywords: G protein-coupled receptor; transmembrane protein  
F15-40/Domain: transmembrane #status predicted <TM1>  
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F189-109/Domain: transmembrane #status predicted <TM3>  
F1133-153/Domain: transmembrane #status predicted <TM4>  
F1177-201/Domain: transmembrane #status predicted <TM5>  
F1227-248/Domain: transmembrane #status predicted <TM6>

F/269-292/Domain: transmembrane #status predicted <TM7>

Query Match 22.8%; Score 367.5; DB 2; Length 308;  
Best Local Similarity 30.3%; Pred. No. 1.1e-26;  
Matches 91; Conservative 64; Mismatches 102; Indels 43; Gaps 10;

QY 10 SSDLTWPPAIKLGFF-AVLGVLLVGLLGLLSLALVFCRCMQWETRIYMTNLAVADLC 68  
DB 3 SSNCSTEDSFYITLYGCVFMSVFLGLJANCVAIYFTFLKVRNETTYTNLNLAISSLL 62

QY 69 LLCTLPFVLHSLRDTSTDP-----LCQLSQGIYLTNRYMSISLTAIAVDYVAVRHPLRA 124  
DB 63 FVFTLPFRIFYF-VVRNWPFGDVLCKISVTLFYTNMYGSLILFLTCISVDRLAIVHPFS 121

QY 125 RGLSRPQAAAVCAVLWVLI-GSLVARWLLGIQEGGFCFRST-RHNFNSMR-----PP- 176  
DB 122 KTLRTKRNARIVCAVMTVLGASTPASF-----FQSTNRQNTTEORTCFENPFE 171

QY 177 -----LLGFYLPVAVVFCPSLKVVVVTALAQRPPTDVGAETRAKAKWYWA 221  
DB 172 STWKYLSRIVIFIEIVGFFIPLIINVTCTMTVLT-LNKPLTLNRNKLKKKVKLMIFV 230

QY 222 NLLVFWVFCFLPHVGL---TVRLAVGNACALLETTIRALYITSKLSDANCLDAICYVY 278  
DB 231 HLIVFCFCFVFNITLILYSLMRTQTWINCSTVAVRTWYPTVTLCAVSNCCFPIVYVF 290

RESULT 4  
T09508  
A>Title: purinergic receptor P2Y5 - human  
N/Alternate names: G-protein coupled receptor  
C/Species: Homo sapiens (man)  
C/Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 09-Jul-2004  
C/Accession: T09508  
R/Bohm, S.K.; Trumpp, A.; Khitin, L.M.; Kong, W.; Payan, D.G.; Bunnett, N.W.  
submitted to the EMBL Data Library, April 1997  
A/Description: The human purinergic receptor P2Y5 is encoded in intron 17 of the retinoblastoma gene.  
A/Reference number: Z16705  
A/Accession: T09508  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: mRNA  
A/Residues: 1-344 <BOH>  
A/Cross-references: UNIPROT:P43657; UNIPARC:UPI000005041B; EMBL:AF000546; NID:g2232068; I09508  
C/Genetics:  
A/Map position: 13  
C/Superfamily: ATP receptor P2u  
C/Keywords: G protein-coupled receptor; transmembrane protein

Query Match 22.3%; Score 359.5; DB 2; Length 344;  
Best Local Similarity 29.2%; Pred. No. 7.1e-26;  
Matches 90; Conservative 68; Mismatches 107; Indels 43; Gaps 10;

QY 10 SSDLTWPPAIKLGFAVL-GVLLVGLLGLLSLALVFCRCMQWETRIYMTNLAVADLC 68  
DB 6 SSHCFYNDSPFYITLYGCMFMSVFLGLVSNCAIYFTFLKVRNETTYTNLNLAISSLL 65

QY 69 LLCTLPFVLHSLRDTSTDP-----LCQLSQGIYLTNRYMSISLTAIAVDYVAVRHPLRA 124  
DB 66 FVFTLPFRIFYF-TTRNWPFGDVLCKISVMLFYTNMYGSLILFLTCISVDRLAIVHPFS 124

QY 125 RGLSRPQAAAVCAVLWVLI-GSLVARWLLGIQEGG-----FCFRTRHNFNSMRFP-- 176  
DB 125 KTLRTKRNARIVCAVMTVLGASTPASF-----FQSTNRQNTTEORTCFENPFE 175

QY 177 -----LLGFYLPVAVVFCPSLKVVVVTALAQRPPTDVGAETRAKAKWYWA 221  
DB 176 TWKTYLSRIVIFIEIVGFFIPLIINVTCTMTVLT-LNKPLTLNRNKLKKKVKLMIFV 233

QY 222 NLLVFWVFCFLPHVGLTVRLAVGNWNA---CALLETIRALYITSKLSDANCLDAICYVY 278  
DB 234 HLIVFCFCFVFNITLILYSLMRTQTWINCSTVAVRTWYPTVTLCAVSNCCFPIVYVF 293

QY 279 MAKEFOEA 286





A:Reference number: JH0712; MUID:93038601; PMID:1329734  
A:Accession: JH0712  
A:Molecule type: DNA  
A:Residues: 1-364 <EGG>  
A:Cross-references: UNIPROT:P30411; UNIPARC:UPI000002A4FC; GB:S45489; NID:g256536; PIDN:R; Powell, S.J.; Slynn, G.; Thomas, C.; Hopkins, B.; Briggs, I.; Graham, A.  
Genomics 15, 435-438, 1993  
A:Title: Human bradykinin B2 receptor: nucleotide sequence analysis and assignment to chromosome 15  
A:Reference number: A46022; MUID:93194199; PMID:7916737  
A:Accession: A46022  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-364 <POW>  
A:Cross-references: UNIPARC:UPI000002A4FC; GB:S56772; NID:g298604; PIDN:AAB25765.1; PID:A; Note: sequences extracted from NCBI backbone (NCBIN:127280, NCBI:P127284)  
R; Ma, J.; Wang, D.; Ward, D.C.; Chen, L.; Dessai, T.; Chao, J.; Chao, L.  
Genomics 23, 362-369, 1994  
A:Title: Structure and chromosomal localization of the gene (BDKRB2) encoding human bradykinin receptor  
A:Reference number: A55559; MUID:95137582; PMID:7835885  
A:Accession: A55559  
A:Molecule type: DNA  
A:Residues: 1-364 <MAA>  
A:Cross-references: UNIPARC:UPI000002A4FC; GB:L27594  
R; Hess, J.F.; Borkowski, J.A.; Young, G.S.; Strader, C.D.; Ransom, R.W.  
Biochem. Biophys. Res. Commun. 184, 260-268, 1992  
A:Title: Cloning and pharmacological characterization of a human bradykinin (BK-2) receptor  
A:Reference number: JQ1488; MUID:92231936; PMID:1314587  
A:Accession: JQ1488  
A:Molecule type: mRNA  
A:Residues: 1-364 <HRS>  
A:Cross-references: UNIPARC:UPI000002A4FC; GB:M88714; NID:gl387999; PIDN:AAB02793.1; PID:C; Genetics:  
A:Gene: GDB:BDKRB2  
A:Cross-references: GDB:L35713; OMIM:113503  
A:Map position: 14q32.1-14q32.2  
C:Superfamily: vertebrate rhodopsin  
C:Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane protein  
P:34-56/Domain: transmembrane #status predicted <TM1>  
P:66-92/Domain: transmembrane #status predicted <TM2>  
P:104-127/Domain: transmembrane #status predicted <TM3>  
P:148-171/Domain: transmembrane #status predicted <TM4>  
P:195-221/Domain: transmembrane #status predicted <TM5>  
P:241-266/Domain: transmembrane #status predicted <TM6>  
P:285-309/Domain: transmembrane #status predicted <TM7>  
P:312,380/Binding site: carboxylate (Asn) (covalent) #status predicted  
P:370,237,342/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted  
P:242/Binding site: phosphate (Thr) (covalent) (by protein kinase A) #status predicted  
P:316/Binding site: phosphate (Ser) (covalent) (by protein kinase A) #status predicted

| Query Match           | 19.3% | Score 311.5;  | DB 2;           | Length 364;        |
|-----------------------|-------|---|-----------------|--------------------|
| Best Local Similarity | 27.6% | Pred. No. 2.3e-21;  |                 |                    |
| Matches               | 89;   | Conservative 54;  | Mismatches 128; | Indels 51; Gaps 9; |
| QY                    | 1     | MNGTYNTCGSSDLTW-----PPAIKLGFYAYLGVLLVLGLLNSIALVWFCRMOQW       | 52              |                    |
| DB                    | 11    | LNGTFAQSKCPQVWGLWGLNTIQPP-----FLWVLFVLATLENIFVLSVFCFLHKS      | 62              |                    |
| QY                    | 53    | TETRIYMTNLAVADICLLCTLPVLUHSLRDTSD-----TPLCQLSGIYLTRYMSISLVT   | 108             |                    |
| DB                    | 63    | TVAEIYGLNLAADLILACGPPFWAITISNNFDWLFGETLCRVVNAITSMNLYSSICFLM   | 122             |                    |
| QY                    | 109   | ATAVDYVAVRPLRGLRSRQAAVCAVLW--VLVIGS--LVARWLLIGQEGGCFR         | 164             |                    |
| DB                    | 123   | LVSIDRYLALVKTMSGMRGVRWAKLVSLSYLVGWCTLLSLSPMLVFRTRMKEYSDEG---- | 178             |                    |
| QY                    | 165   | STRHN-----FNSMRFPLLGFLPLAVVVFCSLKVVTTLAQRPTDVGQA              | 209             |                    |
| DB                    | 179   | ---HNVATCIVSPSLINEVFTMLNVVGFLLPLSVITFCTMQIMQVLRNEMQKPEI       | 235             |                    |
| QY                    | 210   | EATRKAQRMVWNLVVFVFCPLHGLVTV-----RLAVGWNAALLETIRALYITSLKS      | 265             |                    |
| DB                    | 236   | QTERATVNLVVLVLLFFICMLPFOISFTPLDTHRLGI--LSSCODERIIDVITQIASPMA  | 294             |                    |

**Qy** 266 DANCCLDAICYWNAKEPQAS 287  
:  
|||:  
**Db** 295 YSNSCLNPLVIVGVGKFRKKS 316  
:  
|||:  
:  
|||:

**RESULT 12**

CORTB2  
bradykinin receptor type B-2 - rat  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 30-Sep-1992 #sequence revision 30-Sep-1992 #text\_change 09-Jul-2004  
C;Accession: A41283; A55079; S47529  
R;McEachern, A.E.; Shelton, E.R.; Bhakta, S.; O'Brien, R.; Bach, C.; Zuppan,  
Proc. Natl. Acad. Sci. U.S.A. 88, 7724-7728, 1991  
A;Title: Expression cloning of a rat B-2 bradykinin receptor.  
A;Reference number: A41283; MUID:91352062; PMID:1715575  
A;Accession: A41283  
A;Molecule type: mRNA  
A;Residues: 1-366 <MCE>  
A;Cross-references: UNIPROT:P25023; UNIPARC:UIP00001708A1; GB:M59967  
R;Pesquero, J.B.; Lindsey, C.J.; Zeh, K.; Paiva, A.C.M.; Ganten, D.; Bader, M.,  
J. Biol. Chem. 269, 26920-26925, 1994  
A;Title: Molecular structure and expression of rat bradykinin B2 receptor gene.  
A;Reference number: A55079; MUID:95014558; PMID:7929432  
A;Accession: A55079  
A;Status: preliminary; not compared with conceptual translation  
A;Molecule type: DNA  
A;Residues: 1-75, 'A', 77-366 <PS>  
A;Cross-references: UNIPARC:UIP0000024AFE; GB:X80187; GB:X80188; GB:X80189; GB:  
R;Wang, D.; Ma, J.; Chao, L.; Chao, J.,  
Biochim. Biophys. Acta 1219, 171-174, 1994  
A;Title: Molecular cloning and sequence analysis of rat bradykinin B(2) receptor  
A;Reference number: S47529; MUID:94368850; PMID:8086459  
A;Accession: S47529  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-366 <WAN>  
A;Cross-references: UNIPARC:UIP00001708A1; EMBL:L26173; NID:G476749; PIDN:AAAG6  
C;Comment: This G protein-coupled receptor binds the nonapeptide bradykinin.  
C;Superfamily: vertebrate rhodopsin  
C;Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; ligand  
F;31-48/Domain: transmembrane #status predicted <TM>  
F;79-96/Domain: transmembrane #status predicted <TM2>  
F;107-126/Domain: transmembrane #status predicted <TM3>  
F;154-170/Domain: transmembrane #status predicted <TM4>  
F;197-215/Domain: transmembrane #status predicted <TM5>  
F;245-261/Domain: transmembrane #status predicted <TM6>  
F;314,182/Binding site: carboxylate (Asn) (covalent) #status predicted  
F;105-186/Disulfide bonds: #status predicted  
F;326/Binding site: palmitate (Cys) (covalent) #status predicted

**Qy** 2 NGTYNTGSSDLTPWPAIKGLGFAYIGLVLLGLLNLSALWVFCCRMQQMTETRIYMTN 61  
|||||:  
|||:  
**Db** 14 NGTFSEVNCPTDEWWSNLNAIQAPFLWLVLLELALENIFVLVSFVCLHKTNCTVAIYLGN 73  
|||||:  
|||:  
**Qy** 62 LAVADLCILCTLPFVHSLRTSD-----TPLCOLSQGIYLTNRYSISLVTAIAVDRYVA 117  
|||||:  
|||:  
**Db** 74 LAGADLIACGLPFVWAITANNFDWLFGEVLCRVVTMIYNLYSSI CFLMLVSIIDRYLA 133  
|||||:  
|||:  
**Qy** 118 VRHPRLRARGLRSPROAAAVALW--VLVIGS--LVARWLLGIQSGGFCFRSTRIN---- 169  
:  
:  
**Db** 134 LVKTMSGMGRRVRWAKLYSLVINSCITLLSSPMLVFRTKMDYREG-----HNVTAT 186  
:  
:  
**Qy** 170 -----FNSMRFPFLGLPYLPLAVVVFCSLKVVATAORPPDVCQAATRAKGM 218  
|||||:  
|||:  
**Db** 187 VIVYPGRSWEVFTNMLNLNVGLPLLSIIITFCTTRIMQVLRNNMKKFKEVTEKATVL 246  
|||||:  
|||:  
**Qy** 219 VWANLLVFVVCPLPHVG--LTVRLAVG-----WNACALLETRIRALYTISKLD---A 267  
|||:  
|||:  
|||:  
|||:

```
Db      247 VLAIVGLFVLCWFPFOISTDLTLRLGLVSGCWN-----ERAVDIVTQISSVAYS 298
Qy      268 NCCLDAICYYMAKEPQBAS 287
Db      299 NSCLNPLVYIVGKRFKKKS 318

RESULT 13
S13638
platelet-activating factor receptor - guinea pig
C:Species: Cavia porcellus (guinea pig)
C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C:Accession: S13638
R:Honda, Z.; Nakamura, M.; Miki, I.; Minami, M.; Watanabe, T.; Seyama, Y.; Okado, H.; To
Nature 349, 342-346, 1991
A:Title: Cloning by functional expression of platelet-activating factor receptor from gu
A:Reference number: S13638; MUID:91101726; PMID:1846231
A:Accession: S13638
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-342 <HON>
A:Cross-references: UNIPROT:P21556; UNIPARC:UPI00001311BE; GB:X56736; NID:G49442; PIDN:Q
A>Note: the species of guinea pig is not identified; in GenBank entry CCPAFREC, release
C:Superfamily: ATP receptor P2u

Query Match      19.1%; Score 309; DB 2; Length 342;
Best Local Similarity 28.2%; Pred. No. 3.6e-21;
Matches 81; Conservative 58; Mismatches 110; Indels 38; Gaps 9;

Qy      29 VLVLLGLLNSLALWVFCRMM---QOWTETRIYMTNLAVADLCCLCTLP--FVLHSLRDT 83
Db      24 IIFVLGIANGVYLWVP-ARLPSPKLNKIKFKNWLTVDADLLFLITPLWIVVYSGNQ 82

Qy      84 SFTP--LCQLSQGIYLTNRYSISLVTATAVDRYVAVRHPRLRARGLSPROQAAVCAVLW 141
Db      83 WELPKPLCNLACGLFPINTYCVSAPLGVITNRFQAKYPIKTAQATTTRKGLALSIVW 142

Qy      142 VLVIGSLVARWLLIQE-----GGFCFSTRHFNFSMRPPL-----LGFYLPILA 185
Db      143 VAIRAA--ASYFLVMDSTNVSNKAGSGNITRCFEHYEGSKRPVLIHICIVLGFIVFL 200

Qy      186 VVVFCSLKVVTALAQRPTDVGQAEATRAKAKMWMANLLVVFVCFPLHVGTLVRLAVGW 245
Db      201 LILFCNLVLIHTLLRQPVQQRNAEVRRLMWMCTVLAVFVICFVPHM-----VQLPW 255

Qy      246 NACAL-----LETIRRALYITSKLSANDCCCLDAICYYYMAKEPQE 285
Db      256 TLAEGLMFPSSNHOAINDAHQVTLCLLSTNCVLDPVVYCFLTKKPK 302

RESULT 14
B57641
G protein-coupled receptor 4 - pig
C:Species: Sus scrofa domestica (domestic pig)
C>Date: 08-Feb-1996 #sequence_revision 08-Feb-1996 #text_change 09-Jul-2004
C:Accession: B57641
R:Mahadevan, M.S.; Baird, S.; Bailly, J.E.; Shutler, G.G.; Sabourin, L.A.; Tsilfidis, C.
Genomics 30, 84-88, 1995
A:Title: Isolation of a novel G protein-coupled receptor (GPR4) localized to chromosome
A:Reference number: A57641; MUID:96129306; PMID:8595909
A:Accession: B57641
A>Status: preliminary; nucleic acid sequence not shown; translation not shown; significa
A:Molecule type: DNA
A:Residues: 1-362 <MAH>
A:Cross-references: UNIPROT:P50132; UNIPARC:UPI000012BA33; GB:U22108; NID:G722282; PIDN:
C:Genetics:
A:Introns: #status absent
C:Superfamily: G protein-coupled receptor 4
C:Keywords: G protein-coupled receptor

Query Match      19.1%; Score 308.5; DB 2; Length 362;
Best Local Similarity 30.6%; Pred. No. 4.3e-21;
Matches 93; Conservative 48; Mismatches 114; Indels 49; Gaps 11;

Db      247 VLAIVGLFVLCWFPFOISTDLTLRLGLVSGCWN-----ERAVDIVTQISSVAYS 298
Qy      268 NCCLDAICYYMAKEPQBAS 287
Db      299 NSCLNPLVYIVGKRFKKKS 318

RESULT 15
S68207
G protein-coupled receptor 6C.1 - human
C:Species: Homo sapiens (man)
C>Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C:Accession: S68207
R:An, S.; Tsai, C.; Goetzl, E.J.
FEBS Lett. 375, 121-124, 1995
A:Title: Cloning, sequencing and tissue distribution of two related G protein-coupled re
A:Reference number: S68207; MUID:96087098; PMID:7498459
A:Accession: S68207
A>Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-362 <ANS>
A:Cross-references: UNIPROT:P46093; UNIPARC:UPI000016A24A; EMBL:U35399; NID:G1015420; PI
C:Superfamily: G protein-coupled receptor 4
C:Keywords: G protein-coupled receptor

Query Match      19.0%; Score 307.5; DB 2; Length 362;
Best Local Similarity 31.0%; Pred. No. 5.3e-21;
Matches 93; Conservative 49; Mismatches 117; Indels 41; Gaps 11;

Qy      2 NGTYNTC---GSSDLTWPPAIKLGFPYAYLGVLLVGLLLNSLALWVFCRMOQWTETRIY 58
Db      3 NHTWEGCHVDSRVDHLFPPSL-----YIFVIGV-GLPTNCLALWAAVYRQVRQRELGVY 55

Qy      59 MTNLAVADLCCLCTLP----FVLHSLRDTSDTPLCOLSQGIYLTNRYSISLVTATAVDR 114
Db      56 LLNLSIADLLYICSLPLWVDYFLHHDNWIHGGPSCKLFGFIYTYNIYISIAFLCCISVDR 115

Qy      115 YVAVRHPRLRARGLSPROQAAVCAVLWVLTGSLVARWLLGIQEGGFCFRST-RHNFNM 173
Db      116 YLVAHPLRFLARLRVKTAVAVSSVVMATLGANSAP--LFHDE---LFRDRYNHTFCFE 170

Qy      174 RPPL-----LGFYLPVAVVFCSLKVVTALAQRPTDVGQAEATRAKAKRMVW 220
Db      171 KFPBEGWVAMNLYRVFVGFPLFPWMLLSYRGILRAVRGVSST---BRQEKAKIKRAL 227

Qy      221 ANLLVVFVCFPLHVGTLVRLAV---GWNACALLETTIRRALYITSKLSANDCCCLDAICY 276
Db      228 SLIAIVVCFAPYHVLLSRSAYILGRPWD--CGFEERVFSAYHSSLAFTSLNCVADPILY 286

Search completed: February 9, 2006, 01:01:14
Job time : 26.5 secs
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GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: February 9, 2006, 00:47:43 ; Search time 165 Seconds

(without alignments)  
1321.262 Million cell updates/sec

Title: US-10-083-168-85

Perfect score: 1615

Sequence: 1 MNGTYNTCGSSDLTWPPAIAK.....AVAPRAKAKHSQDSLCTVLA 309

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt\_05.80.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | ID           | Description        |
|------------|-------|-------------|--------|--------------|--------------------|
| 1          | 1603  | 99.3        | 309    | Q6FHI8_HUMAN | Q6fhi8 homo sapien |
| 2          | 1597  | 98.9        | 309    | Q6FHI8_HUMAN | Q6fhi8 homo sapien |
| 3          | 1597  | 98.9        | 309    | Q6FHI8_HUMAN | Q6fhi8 homo sapien |
| 4          | 1597  | 98.9        | 309    | Q6FHI8_HUMAN | Q6fhi8 homo sapien |
| 5          | 1592  | 98.6        | 308    | Q6FHI8_HUMAN | Q6fhi8 homo sapien |
| 6          | 1123  | 69.5        | 307    | Q6FHI8_HUMAN | Q6fhi8 homo sapien |
| 7          | 1123  | 69.5        | 307    | Q6FHI8_HUMAN | Q6fhi8 homo sapien |
| 8          | 1122  | 69.5        | 307    | Q6FHI8_HUMAN | Q6fhi8 homo sapien |
| 9          | 1108  | 68.6        | 307    | Q6FHI8_HUMAN | Q6fhi8 homo sapien |
| 10         | 416.5 | 25.8        | 305    | Q6FHI8_HUMAN | Q6fhi8 homo sapien |
| 11         | 402   | 24.9        | 370    | Q6FHI8_HUMAN | Q6fhi8 homo sapien |
| 12         | 401   | 24.8        | 370    | Q6FHI8_HUMAN | Q6fhi8 homo sapien |
| 13         | 399   | 24.7        | 370    | Q6FHI8_HUMAN | Q6fhi8 homo sapien |
| 14         | 399   | 24.7        | 370    | Q6FHI8_HUMAN | Q6fhi8 homo sapien |
| 15         | 391   | 24.2        | 370    | Q6FHI8_HUMAN | Q6fhi8 homo sapien |
| 16         | 381.5 | 23.6        | 302    | Q6FHI8_HUMAN | Q6fhi8 homo sapien |
| 17         | 376.5 | 23.3        | 363    | Q6FHI8_HUMAN | Q6fhi8 homo sapien |
| 18         | 374   | 23.2        | 319    | Q6FHI8_HUMAN | Q6fhi8 homo sapien |
| 19         | 369.5 | 22.9        | 387    | Q6FHI8_HUMAN | Q6fhi8 homo sapien |
| 20         | 369.5 | 22.9        | 387    | Q6FHI8_HUMAN | Q6fhi8 homo sapien |
| 21         | 368   | 22.8        | 345    | Q6FHI8_HUMAN | Q6fhi8 homo sapien |
| 22         | 367.5 | 22.8        | 308    | Q6FHI8_HUMAN | Q6fhi8 homo sapien |
| 23         | 366   | 22.7        | 347    | Q6FHI8_HUMAN | Q6fhi8 homo sapien |
| 24         | 360.5 | 22.3        | 296    | Q6FHI8_HUMAN | Q6fhi8 homo sapien |
| 25         | 360.5 | 22.3        | 344    | Q6FHI8_HUMAN | Q6fhi8 homo sapien |
| 26         | 360   | 22.3        | 372    | Q6FHI8_HUMAN | Q6fhi8 homo sapien |
| 27         | 356.5 | 22.1        | 344    | Q6FHI8_HUMAN | Q6fhi8 homo sapien |
| 28         | 355   | 22.0        | 344    | Q6FHI8_HUMAN | Q6fhi8 homo sapien |
| 29         | 354.5 | 22.0        | 344    | Q6FHI8_HUMAN | Q6fhi8 homo sapien |
| 30         | 348.5 | 21.6        | 360    | Q6FHI8_HUMAN | Q6fhi8 homo sapien |
| 31         |       |             |        |              |                    |

32 341 21.1 358 2 Q4SPQ4\_TETNG Q4spq4 tetraodon n  
33 337.5 20.9 360 2 Q80239\_RAT Q80239 rattus norv  
34 330 20.4 298 2 Q8VE54\_MOUSE Q8ve54 mus musculu  
35 329.5 20.4 374 1 P2RY2\_RAT P41232 rattus norv  
36 328.5 20.3 377 1 P2RY2\_HUMAN P41231 homo sapien  
37 327 20.2 345 2 Q4VENI\_HUMAN Q4vbnl homo sapien  
38 326 20.2 323 2 Q5XGS6\_XENILA Q5xgc0 xenopus lae  
39 326 20.2 346 1 GPR81\_HUMAN Q9bxc0 homo sapien  
40 321.5 19.9 345 1 CLTR2\_PIG Q95n03 sus scrofa  
41 320 19.8 349 2 Q6P852\_XENTR Q6p852 xenopus tro  
42 319.5 19.8 343 1 GPR81\_MOUSE Q8c131 mus musculu  
43 319.5 19.8 361 1 P2RY4\_RAT Q35811 rattus norv  
44 318.5 19.7 365 2 Q4VBB7\_HUMAN Q4vbb7 homo sapien  
45 317.5 19.7 373 2 Q5YA25\_PIG Q5ya25 sus scrofa

#### ALIGNMENTS

##### RESULT 1

ID Q6FHI8\_HUMAN PRELIMINARY; PRT; 309 AA.  
AC Q6FHI8;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DE GPR35 protein.  
GN Name=GPR35;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Halleck A., Ebert L., Moundinya M., Schick M., Eisenstein S.,  
RA Neubert P., Kstrang K., Schatten R., Shen B., Henze S., Mar W.,  
RA Korn B., Zuo D., Hu Y., LaBaer J.;  
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).  
CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.  
CC EMBL; CR541765; BAG46564.1; -; mRNA.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.  
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.  
DR InterPro; IPR000276; GPCR\_Rhodopsn.  
DR PRINTS; PR00237; GPCR\_Rhodopsn.  
DR PROSITE; PS00237; G-PROTEIN RECP\_F1\_1; 1.  
DR PROSITE; PS0262; G-PROTEIN RECP\_F1\_2; 1.  
KW G-protein coupled receptor; Receptor; Transducer; Transmembrane.  
SQ SEQUENCE 309 AA; 34141 MW; FC034FB7231B26F1 CRC64;

Query Match 99.3%; Score 1603; DB 2; Length 309;  
Best Local Similarity 99.4%; Pred. NO. 7.1e-112;  
Matches 307; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MNGTYNTCGSSDLTWPPAIAKLGFAVLGVLLGLLSLALWVFCRCMQQTETRIYMT 60  
Db 1 MNGTYNTCGSSDLTWPPAIAKLGFAVLGVLLGLLSLALWVFCRCMQQTETRIYMT 60  
QY 61 NLAVADLCCLCTLPVLSHSLRDTSTPLCQSQGLYLTNRVMSISLVTAIAVDVAVVRH 120  
Db 61 NLAVADLCCLCTLPVLSHSLRDTSTPLCQSQGLYLTNRVMSISLVTAIAVDVAVVRH 120  
QY 121 PLRAGLRSPQAAACAVLWVLTGSLVARWLLGIQEGGFCFRSTRHNFNSMRPFLG 180  
Db 121 PLRAGLRSPQAAACAVLWVLTGSLVARWLLGIQEGGFCFRSTRHNFNSMRPFLG 180  
QY 181 YLPLAVVFCSLKVVYVTAALQRPPTDVGQAEATKAKRMWVNLVYVVCFLPLHVLTVR 240  
Db 181 YLPLAVVFCSLKVVYVTAALQRPPTDVGQAEATKAKRMWVNLVYVVCFLPLHVLTVR 240

QY 241 LAVGNACALLETIRRALYITSKSDANCLDAICYYWAKEFQEQASALAVAPRAKAKHS 300  
 DB 241 LAVGNACALLETIRRALYITSKSDANCLDAICYYWAKEFQEQASALAVAPRAKAKHS 300  
 QY 301 QDSLVCVTLA 309  
 DB 301 QDSLVCVTLA 309

RESULT 2  
 GPR35 HUMAN  
 ID GPR35 HUMAN STANDARD; PRT; 309 AA.  
 AC Q9HC97; O43495; O86UR4;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 13-SEP-2005 (Rel. 48, Last sequence update)  
 DT 13-SEP-2005 (Rel. 48, Last annotation update)  
 DE Probable G-protein coupled receptor 35.  
 GN Name=GPR35;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
 OC Homo.  
 OC NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE, AND VARIANT ARG-294.  
 RX MEDLINE=98140132; PubMed=9479505; DOI=10.1006/geno.1998.5095;  
 RA O'Dowd B.F., Nguyen T., Marchese A., Cheng R., Lynch K.R.,  
 RA Heng H.H.Q., Kolakowski L.F. Jr., George S.R.;  
 RT "Discovery of three novel G-protein-coupled receptor genes";  
 RL Genomics 47:310-313(1998).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE, AND VARIANTS THR-25; ILE-29; MET-108; SER-125 AND  
 RP MET-253.  
 RX MEDLINE=20472315; PubMed=11017071; DOI=10.1038/79876;  
 RA Horikawa Y., Oda N., Cox N.J., Li X., Orho-Melander M., Hara M.,  
 RA Hinokio Y., Lindner T.H., Mashima H., Schwarz P.E.H.,  
 RA del Bosque-Plata L., Horikawa Y., Oda Y., Yoshiuchi I., Collila S.,  
 RA Polonsky K.S., Wei S., Concannon P., Iwasaki N., Schulze J.,  
 RA Baier L.J., Bogardus C., Groop L., Boerwinkle E., Hanis C.L.,  
 RA Bell G.I.;  
 RT "Genetic variation in the gene encoding calpain-10 is associated with  
 RT type 2 diabetes mellitus";  
 RL Nat. Genet. 26:163-175(2000).  
 RN [3]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].  
 RA Warren C.N., Aronstam R.S., Sharma S.V.;  
 RT "cDNA clones of human proteins involved in signal transduction  
 RT sequenced by the Guthrie cDNA resource center (www.cdna.org).";  
 RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: Orphan receptor.  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).  
 CC -!- TISSUE SPECIFICITY: Expressed in all adult and fetal tissues  
 CC examined, including pancreatic islets and skeletal muscle, with  
 CC relatively higher levels in adult lung, small intestine, colon and  
 CC stomach.  
 CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.  
 CC  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use as long as its content is in no way modified and this statement is not  
 CC removed.

EMBL; AF027957; AAC52028.1; -; Genomic DNA.  
 EMBL; AF089087; AAG17965.1; -; mRNA.  
 EMBL; AY275467; AAP32299.1; -; Genomic DNA.  
 Ensembl; ENSG00000178623; Homo sapiens.  
 HGNC; HGNC:4492; GPR35.  
 MIM; 602646; -.  
 GO; GO:0005887; C:integral to plasma membrane; TAS.  
 GO; GO:0004930; F:G-protein coupled receptor activity; TAS.  
 GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; TAS.  
 InterPro; IPR00276; GPCR\_Rhodopsin.

PFam; PF00001; 7tm 1; 1.  
 PRINTS; PR00237; GPCRHOPOPSN.  
 PROSITE; PS00237; G-PROTEIN RECEPTOR FL1; 1.  
 PROSITE; PS00262; G-PROTEIN RECEPTOR FL2; 1.  
 KW G-protein coupled receptor; Glycoprotein; Polymorphism; Receptor;  
 KW Transducer; Transmembrane.  
 FT TOPO\_DOM 1 24 Extracellular (Potential).  
 FT TRANSMEM 25 45 1 (Potential).  
 FT TOPO\_DOM 46 56 Cytoplasmic (Potential).  
 FT TRANSMEM 57 77 2 (Potential).  
 FT TOPO\_DOM 78 90 Extracellular (Potential).  
 FT TRANSMEM 91 112 3 (Potential).  
 FT TOPO\_DOM 113 135 Cytoplasmic (Potential).  
 FT TRANSMEM 136 156 4 (Potential).  
 FT TOPO\_DOM 157 174 Extracellular (Potential).  
 FT TRANSMEM 175 195 5 (Potential).  
 FT TOPO\_DOM 196 218 Cytoplasmic (Potential).  
 FT TRANSMEM 219 239 6 (Potential).  
 FT TOPO\_DOM 240 258 Extracellular (Potential).  
 FT TRANSMEM 259 279 7 (Potential).  
 FT TOPO\_DOM 280 309 Cytoplasmic (Potential).  
 FT CARBOHYD 2 2 N-linked (GlcNAc...) (Potential).  
 FT DISULFID 89 162 By similarity.  
 FT VARIANT 25 25 A -> T.  
 FT VARIANT 29 29 /FTID=VAR\_013601.  
 FT VARIANT 29 29 V -> I.  
 FT VARIANT 108 108 /FTID=VAR\_013602.  
 FT VARIANT 108 108 T -> M.  
 FT VARIANT 125 125 /FTID=VAR\_013603.  
 FT VARIANT 125 125 R -> S.  
 FT VARIANT 253 253 /FTID=VAR\_013604.  
 FT VARIANT 253 253 T -> M.  
 FT VARIANT 294 294 /FTID=VAR\_013605.  
 FT VARIANT 294 294 S -> R.  
 FT CONFLICT 174 174 A -> R (in Ref. 1).  
 SQ SEQUENCE 309 AA; 34072 MW; 97734PB7231B26F0 CRC64;  
 Query Match 98.9%; Score 1597; DB 1; Length 309;  
 Best Local Similarity 99.0%; Pred. NO. 2e-111;  
 Matches 306; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 MNGYNTCGSSDLTPWPPAIAKLGFAVYGLVILVGLLNSLALWVFCRMOQTETRIYMT 60  
 DB 1 MNGYNTCGSSDLTPWPPAIAKLGFAVYGLVILVGLLNSLALWVFCRMOQTETRIYMT 60  
 QY 61 NLAVADLCCLCTLPFVLHSLRDTSDTPLCQLSQGIYLTNRYSISLVTAIAVDVAVRH 120  
 DB 61 NLAVADLCCLCTLPFVLHSLRDTSDTPLCQLSQGIYLTNRYSISLVTAIAVDVAVRH 120  
 QY 121 PLRARGLSRQAAAVCAVLAQRPPTDVGQAEATRAKRMVWNLVVFVCFPLHVLTVR 180  
 DB 121 PLRARGLSRQAAAVCAVLAQRPPTDVGQAEATRAKRMVWNLVVFVCFPLHVLTVR 180  
 QY 191 YLPLAVVVFCSLVKVTALAQRPTDVGQAEATRAKRMVWNLVVFVCFPLHVLTVR 240  
 DB 191 YLPLAVVVFCSLVKVTALAQRPTDVGQAEATRAKRMVWNLVVFVCFPLHVLTVR 240  
 QY 241 LAVGNACALLETIRRALYITSKSDANCLDAICYYWAKEFQEQASALAVAPRAKAKHS 300  
 DB 241 LAVGNACALLETIRRALYITSKSDANCLDAICYYWAKEFQEQASALAVAPRAKAKHS 300  
 QY 301 QDSLVCVTILA 309  
 DB 301 QDSLVCVTILA 309

RESULT 3  
 Q42FV2 HUMAN  
 ID Q42FV2 HUMAN PRELIMINARY; PRT; 309 AA.  
 AC Q42FV2;  
 DT 13-SEP-2005 (TRENBLrel. 31, Created)  
 DT 13-SEP-2005 (TRENBLrel. 31, Last sequence update)

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DE 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
OS Hypothetical protein FLJ16773.
OC Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RA Kawakami B., Sugiyama A., Takemoto M., Sugiyama T., Irie R.,
RA Otsuki T., Sato H., Ota T., Wakamatsu A., Ishii S., Yamamoto J.,
RA Isono Y., Kawai-Hio Y., Saio K., Nishikawa T., Kimura K.,
RA Yamashita H., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,
RA Wagatsuma M., Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A.,
RA Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.;
RA Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
RL SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
DR EMBL; AK131540; BADI8676.1; -; mRNA.
DR Ensembl; ENSG00000178623; Homo sapiens.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; P:receptor activity; IEA.
DR GO; GO:0001584; P:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHHODOPS.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
DR KW G-protein coupled receptor; Receptor; Transducer; Transmembrane.
SQ SEQUENCE 394 AA; 43309 MW; 1598FD44BAE4233C CRC64;

Query Match 98.9%; Score 1597; DB 2; Length 394;
Best Local Similarity 99.0%; Pred. No. 2.5e-111;
Matches 306; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MNGTYNTCGSSDLTWPPAIKLGFYAYLGVLVGLLNSLALWVFCRMOQWTTETRYMT 60
DB 86 MNGTYNTCGSSDLTWPPAIKLGFYAYLGVLVGLLNSLALWVFCRMOQWTTETRYMT 145

QY 61 NLAVADICLLCTLPFVLHSLRDTSDTPLCQLSQGIYLTNRYSISLVTAIAVDRYAVRH 120
DB 146 NLAVADICLLCTLPFVLHSLRDTSDTPLCQLSQGIYLTNRYSISLVTAIAVDRYAVRH 205

QY 121 PLRAGLRSPROAAVCAVAVLVIGSLVARWLLGIQGGFCFRSTRHNFNSMFPPLIGF 180
DB 206 PLRAGLRSPROAAVCAVAVLVIGSLVARWLLGIQGGFCFRSTRHNFNSMFPPLIGF 265

QY 181 YLPLAVVVFCSLKVVTTALAQRPPTDVQAEATRAKRWANLVVFCFLPLHVLTVR 240
DB 266 YLPLAVVVFCSLKVVTTALAQRPPTDVQAEATRAKRWANLVVFCFLPLHVLTVR 325

QY 241 LAVGNACALLETIRRALYITTSKLSANDCCLDICYYTMAKEFOEASALAVAPRAKAHS 300
DB 326 LAVGNACALLETIRRALYITTSKLSANDCCLDICYYTMAKEFOEASALAVAPRAKAHS 385

QY 301 QDSLCTVLA 309
DB 386 QDSLCTVLA 394

RESULT 5
Q4VBN5 HUMAN PRELIMINARY; PRT; 308 AA.
ID Q4VBN5
AC Q4VBN5;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE GPR35 protein (Fragment).
GN Name=GPR35;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

DE 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
OS Hypothetical protein GPR35.
OC Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RA Haakenson W., Trani L., Schatzkammer K.;
RA "The sequence of Homo sapiens BAC clone RP11-27M15.";
RA Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
RL SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
DR EMBL; AC124862; AX88945.1; -; Genomic_DNA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHHODOPS.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
DR KW G-protein coupled receptor; Hypothetical protein; Receptor; Transducer; Transmembrane.
SQ SEQUENCE 309 AA; 34072 MW; 97734FB7231B26F0 CRC64;

Query Match 98.9%; Score 1597; DB 2; Length 309;
Best Local Similarity 99.0%; Pred. No. 2e-111;
Matches 306; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MNGTYNTCGSSDLTWPPAIKLGFYAYLGVLVGLLNSLALWVFCRMOQWTTETRYMT 60
DB 1 MNGTYNTCGSSDLTWPPAIKLGFYAYLGVLVGLLNSLALWVFCRMOQWTTETRYMT 60

QY 61 NLAVADICLLCTLPFVLHSLRDTSDTPLCQLSQGIYLTNRYSISLVTAIAVDRYAVRH 120
DB 61 NLAVADICLLCTLPFVLHSLRDTSDTPLCQLSQGIYLTNRYSISLVTAIAVDRYAVRH 120

QY 121 PLRAGLRSPROAAVCAVAVLVIGSLVARWLLGIQGGFCFRSTRHNFNSMFPPLIGF 180
DB 121 PLRAGLRSPROAAVCAVAVLVIGSLVARWLLGIQGGFCFRSTRHNFNSMFPPLIGF 180

QY 181 YLPLAVVVFCSLKVVTTALAQRPPTDVQAEATRAKRWANLVVFCFLPLHVLTVR 240
DB 181 YLPLAVVVFCSLKVVTTALAQRPPTDVQAEATRAKRWANLVVFCFLPLHVLTVR 240

QY 241 LAVGNACALLETIRRALYITTSKLSANDCCLDICYYTMAKEFOEASALAVAPRAKAHS 300
DB 241 LAVGNACALLETIRRALYITTSKLSANDCCLDICYYTMAKEFOEASALAVAPRAKAHS 300

QY 301 QDSLCTVLA 309
DB 301 QDSLCTVLA 309

RESULT 4
Q6ZMP9 HUMAN PRELIMINARY; PRT; 394 AA.
ID Q6ZMP9
AC Q6ZMP9;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
 OC Homo.  
 RN NCBI\_TaxID=9606;  
 RN [1]  
 RC NUCLEOTIDE SEQUENCE.  
 RP TISSUE=G-protein coupled receptors;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Krausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Krausberg R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,  
 RA Altschul S.F., Zebrow B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [2]  
 RN NUCLEOTIDE SEQUENCE.  
 RC TISSUE=G-protein coupled receptors;  
 RG NIH MGC Project;  
 RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).  
 CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.  
 DR EMBL; BC095500; AAH95500.1; -; mRNA.  
 DR InterPro; IPR000276; GPCR\_Rhodopsin.  
 DR Pfam; PF00001; 7tm\_1; 1.  
 DR PRINTS; PR00237; GPCRHOOPS.  
 DR PROSITE; PS00237; G PROTEIN RECP F1\_1; 1.  
 DR PROSITE; PS00262; G PROTEIN RECP F1\_2; 1.  
 KW G-protein coupled receptor; Receptor; Transducer; Transmembrane.  
 FT NON\_TER 1  
 FT NON\_TER 308  
 SQ SEQUENCE 308 AA; 33941 MW; 5791BF9CE7206034 CRC64;  
 Query Match 98.6%; Score 1592; DB 2; Length 308;  
 Best Local Similarity 99.0%; Pred. No. 4.7e-111;  
 Matches 305; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 2 NGTYNTCGSDLTWPPAIGFAYILGVLLVGLLNSLALWVFCRMOQWTETRIYMTN 61  
 Db 1 NGTYNTCGSDLTWPPAIGFAYILGVLLVGLLNSLALWVFCRMOQWTETRIYMTN 60  
 QY 62 LAVADICLLCTLPFVLHSLRDTSDTLPCLQSQGIYLTNRYSLSLTAVDRIYAVRHP 121  
 Db 61 LAVADICLLCTLPFVLHSLRDTSDTLPCLQSQGIYLTNRYSLSLTAVDRIYAVRHP 120  
 QY 122 LRARGLSRQAAAVCAVLWVLVIGSLVARWLLGIQGGFCFSTRHFNFSNMFLLGIFY 181  
 Db 121 LRARGLSRQAAAVCAVLWVLVIGSLVARWLLGIQGGFCFSTRHFNFSNMFLLGIFY 180  
 QY 182 LPLAVVVFCSLKVVTALQRPPTDVGQABTRKAKRMVWNLVVFVFCPLPLHVLGTVRL 241  
 Db 181 LPLAVVVFCSLKVVTALQRPPTDVGQABTRKAKRMVWNLVVFVFCPLPLHVLGTVRL 240  
 QY 242 AVGNWACALLETIRRALYITSKLSDANCCLDALCYIYMAKEFOESALAVAPAKAHKQ 301  
 Db 241 AVGNWACALLETIRRALYITSKLSDANCCLDALCYIYMAKEFOESALAVAPAKAHKQ 300  
 QY 302 DSLCVTLA 309  
 Db 301 DSLCVTLA 308

RESULT 6  
 GPR35\_MOUSE  
 ID GPR35\_MOUSE STANDARD; PRT; 307 AA.  
 AC Q9ES90;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DE Probable G-protein coupled receptor 35.  
 GN Name=Gpr35;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muroidae; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=20472315; PubMed=11017071; DOI=10.1038/79876;  
 RA Horioka Y., Oda N., Cox N.J., Li X., Orho-Melander M., Hara M.,  
 RA Hinkio Y., Lindner T.H., Mashima H., Schwarz P.E.H.,  
 RA del Bosque-Plata L., Horioka Y., Oda Y., Yoshiuchi I., Colilla S.,  
 RA Polonsky K.S., Wei S., Concannon P., Iwasaki N., Schulze J.,  
 RA Baier L.J., Bogardus C., Groop L., Boerwinkle E., Hanis C.L.,  
 RA Bell G.I.;  
 RT "Genetic variation in the gene encoding calpain-10 is associated with  
 RT type 2 diabetes mellitus.";  
 RL Nat. Genet. 26:163-175 (2000).  
 RN [2]  
 RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].  
 RC STRAIN=C57BL/6J; TISSUE=Mammary gland;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Krausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Krausberg R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,  
 RA Altschul S.F., Zebrow B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 CC -1- FUNCTION: Orphan receptor.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).  
 CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
 CC EMBL; AF200349; AAG18487.1; -; mRNA.  
 CC EMBL; BC027429; AAH27429.1; -; mRNA.  
 CC Ensembl; ENSMUSG00000026271; Mus musculus.  
 CC MGI; MGI:1929509; Gpr35.  
 CC GO; GO:0016021; C: integral to membrane; TAS.  
 CC InterPro; IPR000276; GPCR\_Rhodopsin.  
 CC InterPro; IPR002286; P2\_purnocptor.  
 CC Pfam; PF00001; 7tm\_1; 1.  
 CC PRINTS; PR00237; GPCRHOOPS.  
 CC PROSITE; PS00237; G PROTEIN RECP F1\_1; 1.  
 CC PROSITE; PS00262; G PROTEIN RECP F1\_2; 1.  
 CC PROSITE; PS0262; G\_PROTEIN\_RECP\_F1\_2; 1.



ARAKAWA T., HARA A., FUKUNISHI Y., KONNO H., ADACHI J., FUKUDA S.,  
 AIZAWA K., IZAWA M., NISHI K., KIYOSAWA H., KONDO S., YAMANAKA I.,  
 SAITO T., OKAZAKI Y., GOJOBOI T., BONO H., KASUKAWA T., SAITO R.,  
 KADOTA K., MATSUDA H.A., ASHBURNER M., BATALOV S., CASAVANT T.,  
 FLEISCHMANN W., GAESTERLAND T., GIESI C., KING B., KOCHIWA H.,  
 KUEHL P., LEWIS S., MATSUO Y., NIKAI D., PESOLE G., QUACKENBUSH J.,  
 SCHIRML L.M., STAUBLI F., SUZUKI R., TOMITA M., WAGNER L., WASHIO T.,  
 SAKAI K., OKIDO T., FURUNO M., ANO H., BALDARELLI R., BARSH G.,  
 BLAKE J., BOFFELLI D., BOJUNGA N., CARNINCI P., DE DONALDO M.F.,  
 BROWNSTEIN M.J., BULT D., HOFMANN C., FUJITA M., GARIBOLDI M.,  
 GUSTINCICH S., HILL D., HOFMANN C., HUME D.A., KAMIYA M., LEE N.H.,  
 LYONS P., MARCHIONNI L., MASHIMA J., MAZZARELLI J., MOMBARTS P.,  
 NORDONE P., RING B., RINGWALD M., RODRIGUEZ I., SAKAMOTO N.,  
 SASAKI H., SATO K., SCHOENBACH C., SEYA T., SHIBATA Y., STORCH K.-F.,  
 SUZUKI H., TOYO-OKA K., WANG K.H., WEITZ C., WHITTAKER C., WILMING L.,  
 WYNNEBOW-BORIS A., YOSHIDA K., HASEGAWA Y., KAWAJI H., KOHTEUKI S.,  
 HAYASHIZAKI Y.,  
 "Functional annotation of a full-length mouse cDNA collection.";  
 Nature 409:685-690(2001).  
 [3]  
 NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J; TISSUE=Bone;  
 RA The FANTOM Consortium,  
 RA "Analysis of the mouse transcriptome based on functional annotation of  
 60,770 full-length cDNAs.";  
 RT Nature 420:563-573(2002).  
 RL [4]  
 NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J; TISSUE=Bone;  
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;  
 RA Carninci P., Shibata Y., Hayatsu M., Sugahara Y., Shibata K., Itoh M.,  
 KONNO H., OKAZAKI Y., MURAMATSU M., HAYASHIZAKI Y.,  
 "Normalization and subtraction of cap-trapper-selected cDNAs to  
 prepare full-length cDNA libraries for rapid discovery of new genes.";  
 Genome Res. 10:1617-1630(2000).  
 [5]  
 NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J; TISSUE=Bone;  
 RX MEDLINE=20530913; PubMed=11076961; DOI=10.1101/gr.152600;  
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,  
 KONNO H., AKIYAMA J., NISHI K., KITSUMAI T., TASHIRO H., ITOH M.,  
 SUMI N., ICHII Y., NAKAMURA S., HAZAMA M., NISHINE T., HARADA A.,  
 YAMAMOTO R., MATSUMOTO H., SAKAGUCHI S., ISEGAMI T., KASHIWAGI K.,  
 FUJIIWAKE S., INOUE K., TOGAWA Y., IZAWA M., OHARA E., WATAHIKI M.,  
 YONEDA Y., ISHIKAWA T., OZAWA K., TANAKA T., MATSUURA S., KAWAI J.,  
 OKAZAKI Y., MURAMATSU M., INOUE Y., KIRA A., HAYASHIZAKI Y.,  
 "RIKEN integrated sequence analysis (RISA) system-384-format  
 sequencing pipeline with 384 multicapillary sequencer.";  
 Genome Res. 10:1757-1771(2000).  
 [6]  
 NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J; TISSUE=Bone;  
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,  
 FUKUDA S., FURUNO M., HANAGAKI T., HARA A., HASHIZUME W.,  
 HAYASHIDA K., HAYATSU N., HIRAMOTO K., HIRAOKA T., HIROZANE T.,  
 HORI F., INOTANI K., ISHII Y., ITOH M., KAGAWA I., KASUKAWA T.,  
 KATO H., KAWAI J., KOJIMA Y., KONDO S., KONNO H., KODA M., KOYA S.,  
 KURIHARA C., MATSUYAMA T., MIYAZAKI A., MURATA M., NAKAMURA M.,  
 NISHI K., NOMURA K., NUNAKAZI R., OHNO M., OHSATO N., OKAZAKI Y.,  
 SAITO R., SAITOH H., SAKAI C., SAKAI K., SAKAZUME N., SANO H.,  
 SASAKI D., SHIBATA K., SHINGAWA A., SHIRAKI T., SOGABE Y., TAGAMI M.,  
 TAGAWA A., TAKAHASHI F., TAKAKU-AKASHIRA S., TAKEDA Y., TANAKA T.,  
 TOMARU A., TOYA T., YASUNISHI A., MURAMATSU M., HAYASHIZAKI Y.,  
 Submitted (JUL-2001) to the EMBL/GenBank/DBJ database.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (by similarity).  
 CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.  
 DR EMBL; AK036503; BAC29453.1; -; mRNA.  
 DR MGI; MGI:1929509; Gpr35.  
 DR GO; GO:0016021; C:integral to membrane; TAS.  
 DR InterPro; IPR000276; GPCR Rhodopsin.  
 DR InterPro; IPR002286; P2\_purnocptor.  
 DR Pfam; PF00001; 7tm\_1; 1.

DR PRINTS; PR002137; GPCRHOOPS.  
 DR PRINTS; PR01157; P2YFURNOCPTR.  
 DR PROSITE; PS00337; G-PROTEIN RECEPTOR FL1; 1.  
 DR PROSITE; PS00362; G-PROTEIN RECEPTOR FL2; 1.  
 KW G-protein coupled receptor; Receptor; Transducer; Transmembrane.  
 SQ SEQUENCE 307 AA; 34140 MW; 8EB439A9D5P7656 CRC64;  
 Query Match 69.5%; Score 1122; DB 2; Length 307;  
 Best Local Similarity 71.9%; Pred. No. 6.2e-76;  
 Matches 223; Conservative 30; Mismatches 51; Indels 6; Gaps 5;  
 QY 1 MNGTYNTGSSDLTPWPAKLGKFGYVGLVLLVGLLLNSLALWVFCRMOQWTTETRIYMT 60  
 DB 1 MNST--TCNST-LTWPAVSNVFFTYISALLVGLLLNSVALWVFCYRQHQWTTETRIYMT 57  
 QY 61 NLAVADLCCLCTLPFLVLSLR-DTSDTPLCQLSQGIYLTNRYSISLVTAIVADRYVAVR 119  
 DB 58 NLAVADLCCLCSLPFLVLSKYSSDTPVQQLSQGIYLTNRYSISLVTAIVADRYVAVR 117  
 QY 120 HPLRARGLRSPQAAAACVAVLVVGLSVARWLGIQEGGFCFRS-TRHNSNMRFPPLL 178  
 DB 118 HPLRARELRSPQAAAACVAVLVVGLSVARWLGMQEGGFCFRSQTFRNFSTTAFSL 177  
 QY 179 GPYLPVAVVFCSLKVVLTALQRPPTDVGQAEATKAKEMVWNLVVFVVCFLPLHVGIT 238  
 DB 178 GPYLPVAVVFCSLQVVTLSRPAADVGQAEATKATMVMWNLVAVFVICFLPLHVL 237  
 QY 239 VRLAVGNACALLETIRBALYITSKLSDANCCLDCAICYYMAKBFQASALAVAPRAKAH 298  
 DB 238 VQVSLNLTNCAARDTPSRALSITGKLSNTNCLDCAICYYMAKBFQASALAVAPRAKAH 296  
 QY 299 KSQDSLCVTL 308  
 DB 297 KSQDSQILSL 306  
 RESULT 9  
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 ID QBBS98; Q8BS98;  
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Mus musculus 12 days embryo embryonic body between diaphragm region  
 DE and neck cDNA, RIKEN full-length enriched library, clone:9430051L15  
 DE product:G protein-coupled receptor 35, full insert sequence.  
 GN Name=Gpr35;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]\_NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J;  
 RC TISSUE=Embryonic body between diaphragm region and neck;  
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;  
 RA Carninci P., Hayashizaki Y.;  
 RT "High-efficiency full-length cDNA cloning.";  
 RL Meth. Enzymol. 303:19-44(1999).  
 [2]  
 NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J;  
 RC TISSUE=Embryonic body between diaphragm region and neck;  
 RX MEDLINE=11217851; PubMed=11217851; DOI=10.1038/35055500;  
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
 ARAKAWA T., HARA A., FUKUNISHI Y., KONNO H., ADACHI J., FUKUDA S.,  
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 SCHIRML L.M., STAUBLI F., SUZUKI R., TOMITA M., WAGNER L., WASHIO T.,

RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barash G.,  
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
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RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,  
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohzuki S.,  
RA Hayaishizaki Y.;  
RT "Functional annotation of a full-length mouse cDNA collection.";  
RL Nature 409:685-690(2001).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J;  
RC TISSUE=Embryonic body between diaphragm region and neck;  
RA The FANTOM Consortium,  
RA the RIKEN Genome Exploration Research Group Phase I & II Team;  
RT "Analysis of the mouse transcriptome based on functional annotation of  
RT 60,770 full-length cDNAs.";  
RL Nature 420:563-573(2002).  
RN [4]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J;  
RC TISSUE=Embryonic body between diaphragm region and neck;  
RX MEDLINE=20493374; PubMed=11042159; DOI=10.1101/gr.145100;  
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,  
RA Konno H., Okazaki Y., Muramatsu M., Hayaishizaki Y.;  
RT "Normalization and subtraction of cap-trapper-selected cDNAs to  
RT prepare full-length cDNA libraries for rapid discovery of new genes.";  
RL Genome Res. 10:1617-1630(2000).  
RN [5]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J;  
RC TISSUE=Embryonic body between diaphragm region and neck;  
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;  
RA Shibata K., Itoh M., Aizawa K., Nagao K., Sasaki N., Carninci P.,  
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,  
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada K.,  
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RT "RIKEN integrated sequence analysis (RISA) system-384-format  
RT sequencing pipeline with 384 multicapillary sequencer.";  
RL Genome Res. 10:1757-1771(2000).  
RN [6]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J;  
RC TISSUE=Embryonic body between diaphragm region and neck;  
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,  
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,  
RA Hayaishida K., Hayatsu N., Hiramoto K., Hiraoka I., Kasukawa T.,  
RA Horii F., Imotani K., Iehii Y., Itoh M., Kagawa I., Kouda M., Koya S.,  
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Kura  
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RA Saito K., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,  
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,  
RA Tagawa A., Takahashi F., Takaku-Akaira S., Takeda Y., Tanaka T.,  
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayaishizaki Y.;  
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).  
CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.  
DR EMBL; AK034870; BAC28861.1; -; mRNA.  
DR MGI; MGI:1929509; Gpr35.  
DR GO; GO:0016021; C:integral to membrane; TAS.  
DR InterPro; IPR000276; GPCR\_Rhodpsn.  
DR InterPro; IPR002286; P2\_purinocpt.  
DR Pfam; PF00001; 7tm 1; 1.  
DR PRINTS; PR00237; GPCR\_Rhodopsn.  
DR PRINTS; PR01157; P2PURNOCPT.  
DR PROSITE; PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.

DR PROSITE; PS00262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
KW G-protein coupled receptor; Receptor; Transducer; Transmembrane.  
SQ SEQUENCE 307 AA; 34260 MW; 923D02CECB0D70AC CRC64;  
Query Match 68.6%; Score 1108; DB 2; Length 307;  
Best Local Similarity 71.3%; Pred. No. 6.9e-75;  
Matches 221; Conservative 30; Mismatches 53; Indels 6; Gaps 5;  
QY 1 MNGTYNTGSSDLTWPPAIKLGFIYVGLVLLVGLLNSLALWVFCRMOQMTETRIYMT 60  
DB 1 MNST--TCNST-LTWPAVNNFIYSALLVGLLNSVALWVFCVHMQMTETRIYMT 57  
QY 61 NLAVADLCLLCTLPFVLSLR-DTSDPLCQLSQGIYLTNRYMSISLVTAIVDRYAVR 119  
DB 58 NLAVADLCLLCSLPFVLSLYKSSDTPVQSLSQGIYLTNRYMSISLVTAIVDRYAVR 117  
QY 120 HPLRARGLSRQAAAVCAVLVTVGLSVARWLLGIQSGGFCFRS-TRNFNSMRPPLL 178  
DB 118 HPLRARELSRQAAAVCAVVALWVTVSLVVRWLGWQGGFCFSQTRNRFSTTAFSL 177  
QY 179 GFYLPVAVVFCSLKVVTALAQRPPTDVGQAETRAKRMVWNLVVFVVCFLPHVGLT 238  
DB 178 GFYLPVAVVFCSLQVTVLSRPAADVQAETQKATMVWNLVAVFVICFLPHVGLT 237  
QY 239 VRLAVGNACALLETTRRLRYITSKLSDANCLDAICYYMAKEFOEASALAVPRAK 298  
DB 238 VQVSLNLTCAARDTFSRLSITGKLSLSDTNCLDAICYYMAREFOEAFKPAYSSNT-PH 296  
QY 299 KSQDSLCVTL 308  
DB 297 KSQYSQILSL 306  
RESULT 10  
Q4TAHO TESTNG PRELIMINARY; PRT; 305 AA.  
AC Q4TAHO;  
DT 13-SEP-2005 (T-EMBLrel. 31, Created)  
DT 13-SEP-2005 (T-EMBLrel. 31, Last sequence update)  
DT 13-SEP-2005 (T-EMBLrel. 31, Last annotation update)  
DE Chromosome 1 SCAF7335, whole genome shotgun sequence. (Fragment).  
GN ORFNames=GSTENG00004207001;  
OS Tetraodon nigroviridis (Green puffer).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;  
OC Tetraodontidae; Tetraodontidae; Tetraodon.  
OX NCBI\_TaxID=99883;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,  
RA Mauceli E., Bouteau L., Fischer C., Ozouf-Costaz C., Bernot A.,  
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RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,  
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RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals  
RT the early vertebrate proto-karyotype.";  
RL Nature 431:946-957(2004).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC Genoscope; Whitehead Institute Centre for Genome Research;  
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.  
CC -!- CAUTION: The sequence shown here is derived from an  
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
CC preliminary data.  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).







RA O'Dowd B.F., Nguyen T., Jung B.P., Marchese A., Cheng R., Heng H.H.Q.,  
RA Kolakowski L.F. Jr., Lynch K.R., George S.R.;  
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RT protein-coupled receptor genes.";  
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RX MEDLINE=9736605; PubMed=9223435; DOI=10.1006/bbrc.1997.6895;  
RA Janssens R., Boeynaems J.M., Godart M., Communi D.;  
RT "Cloning of a human heptahelical receptor closely related to the P2Y5  
RT receptor";  
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RA Kopatz S.A., Aronstam R.S., Sharma S.V.;  
RT "cDNA clones of human proteins involved in signal transduction  
RT sequenced by the Guthrie cDNA resource center (www.cdna.org).";  
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[5]  
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RX PubMed=15772651; DOI=10.1038/nature03440;  
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RA Woodmansey R.L., Wray P.W., Yen J., Zhang J., Zhou J., Zoghbi H.,

RA Zorilla S., Buck D., Reinhardt R., Poustka A., Rosenthal A.,  
RA Lehrach H., Meindl A., Minx P.J., Hillier L.W., Willard H.F.,  
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RA Gibbs R.A., Beck S., Rogers J., Bentley D.R.;  
RT "The DNA sequence of the human X chromosome.";  
RL Nature 434:325-337(2005).  
[6]  
RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].  
RP TISSUE=Brain;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zerborg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
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RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,  
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RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
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RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
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RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,  
RA Schnarch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RL and mouse cDNA sequences.";  
CC Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -1- TISSUE SPECIFICITY: Not detected in the brain regions thalamus,  
CC putamen, caudate, frontal cortex, pons, hypothalamus and  
CC hippocampus.  
CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.  
CC  
CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use as long as its content is in no way modified and this statement is not  
CC removed.  
CC  
CC EMBL; U66578; AAC51301.1; -; Genomic DNA.  
CC EMBL; U90323; AAB62087.1; -; Genomic DNA.  
CC EMBL; U90322; AAB62088.1; -; mRNA.  
CC EMBL; AF005419; AAB66322.1; -; Genomic DNA.  
CC EMBL; AY301274; AAP58404.1; -; Genomic DNA.  
CC EMBL; AL590083; CAD18851.1; -; Genomic DNA.  
CC EMBL; BC074722; AAH74722.1; -; mRNA.  
CC PIR; JC5549; JCS5549.  
CC HSP; P34996; IDDD.  
CC Ensembl; ENSG00000147145; Homo sapiens.  
CC HGNC; HGNC:4478; GPR23.  
CC  
CC GO; GO:0005887; C: integral to plasma membrane; TAS.  
CC GO; GO:0004930; P: G-protein coupled receptor activity; TAS.  
CC GO; GO:0007186; P: G-protein coupled receptor protein signalin. .; TAS.  
CC InterPro; IPR000276; GPCR\_Rhodopsn.  
CC InterPro; IPR002188; P2Y5\_purinceptor.  
CC Pfam; PF00001; 7tm.1; 1.  
CC PRINTS; PR00237; GPCR\_Rhodopsn.  
CC PRINTS; PR01067; P2Y5ORPHAN.  
CC PROSITE; PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.  
CC PROSITE; PS00262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
CC G-protein coupled receptor; Glycoprotein; Receptor; Transducer;  
KW Transmembrane. 1 43 Extracellular (Potential).  
KW TOPO\_DOM 44 64 1 (Potential).  
KW TRANSMEM 45 73 Cytoplasmic (Potential).  
KW TOPO\_DOM 65 94 2 (Potential).  
KW TRANSMEM 76 112 Extracellular (Potential).  
KW TOPO\_DOM 95 113 3 (Potential).  
KW TRANSMEM 113 133



GN Name=Gpr23;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Spinal ganglion;  
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;  
RA Carninci P., Hayashizaki Y.;  
RT "High-efficiency full-length cDNA cloning.";  
RL Meth. Enzymol. 303:19-44(1999).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Spinal ganglion;  
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;  
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
RA Akazawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
RA Akazawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,  
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
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RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-P.,  
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,  
RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,  
RA Hayashizaki Y.;  
RT "Functional annotation of a full-length mouse cDNA collection.";  
RL Nature 409:685-690(2001).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Spinal ganglion;  
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;  
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,  
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;  
RT "Normalization and subtraction of cap-trapper-selected cDNAs to  
prepare full-length cDNA libraries for rapid discovery of new genes.";  
RL Genome Res. 10:1617-1630(2000).  
RN [4]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Spinal ganglion;  
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;  
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,  
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;  
RT "Normalization and subtraction of cap-trapper-selected cDNAs to  
prepare full-length cDNA libraries for rapid discovery of new genes.";  
RN [5]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Spinal ganglion;  
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;  
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,  
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,  
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,  
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RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,  
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,  
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;  
RT "RIKEN integrated sequence analysis (RISA) system-384-format  
sequencing pipeline with 384 multicapillary sequencer.";  
RL Genome Res. 10:1757-1771(2000).  
RN [6]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Spinal ganglion;  
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,  
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,

RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,  
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,  
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,  
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,  
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,  
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,  
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tsgami M.,  
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,  
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;  
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).  
DR EMBL; AK051709; BAC34729.1; -; mRNA.  
DR MGI; MGI:1925384; Gpr23.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0045028; F:purinergic nucleotide receptor activity; G- . . ; IEA.  
DR GO; GO:0004872; F:receptor activity; IEA.  
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.  
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . . ; IEA.  
DR GO; GO:0007165; P:signal transduction; IEA.  
DR InterPro; IPR002188; GPCR Rhodopsin.  
DR InterPro; IPR002188; P2Y5\_purinceptor.  
DR Pfam; PF00001; 7tm.1.1.  
DR PRINTS; PR00237; GPCRHOPOPSN.  
DR PRINTS; PR01067; P2Y5ORPHAN.  
DR PROSITE; PS00237; G PROTEIN RECEPTOR FL1; UNKNOWN\_1.  
DR PROSITE; PS0262; G PROTEIN RECEPTOR FL2; 1.  
KW G-protein coupled receptor; Receptor; Transducer; Transmembrane.  
SQ SEQUENCE 370 AA; 41956 MW; AB126842343AE6E1 CRC64;  
Query Match 24.7%; Score 399; DB 2; Length 370;  
Best Local Similarity 34.3%; Pred. No. 7.9e-22;  
Matches 104; Conservative 59; Mismatches 112; Indels 28; Gaps 11;  
QY 4 TYNTGSSDLTWPAPKLGFPAYLVGLVLLVGLLNSLWVFCRCMQQWETRIYMTNL 62  
DB 27 TNNTICVDD-----SFKNLNGAVYSVVFILGLITNSASLFFVCFRMRKSETAIFITNL 81  
QY 63 AVADLCCLCTLPF-VLHSLR---DTSDTPLCQLSQGIYLTNRNYSISLVTATVADRYVAV 118  
DB 82 ALSDLLFVCTLPFKIFYNFNHWPFGDT-LCKISGTAFLNIYVSMFLTICISVDRLAI 140  
QY 119 RHPRLARGLSPROAAAVCAVWLVIGSLVARMLLQIE-----GGFCFRSTRHN 169  
DB 141 VYFPRSTIRTRNSAIVCAGWILVILNGGSIASLFTSTNNVNNATTTTCFEGSRVWKTY 200  
QY 170 FNSMR--FPLGLFVLPLAVVFCSLKVVTALAQRPPTDVQAEAT-RKAKEMVANLLVF 226  
DB 201 LSKITIFIEVVGFIPLILNVSCSVVLRTL--RKPATLSQIGNKKKVLKMITVHMAVF 258  
QY 227 VVCFPLHVLGLTVRLAVGNAC--ALLETRRALLY-ITSKLSDANCCLDACIYYMAKEF 283  
DB 259 VVCFVFPNSVFLYALVRSQAITNCLLERFAKIMYPITLCLATLNCDFDPFIYFTLESF 318  
QY 284 QEA 286  
DB 319 QKS 321  
RESULT 15  
Q8BLG2 MOUSE  
ID Q8BLG2 MOUSE PRELIMINARY; PRT; 370 AA.  
AC Q8BLG2;  
DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Mus musculus 9.5 days embryo parthenogenote cDNA, RIKEN full-length  
DE enriched library, clone:B130055L15 product:P2Y PURINOCEPTOR 9, full  
DE insert sequence.  
GN Name=Gpr23;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridae; Murinae; Mus.

OK NCBI\_TaxID=10090;  
 RN [1]\_TaxID=10090;  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J; TISSUE=Parthenogenote;  
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;  
 RA Carninci P., Hayashizaki Y.;  
 RT "High-efficiency full-length cDNA cloning.";  
 RL Meth. Enzymol. 303:19-44(1999).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J; TISSUE=Parthenogenote;  
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;  
 RA Kawai J., Shingagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Konno S., Yamada I.,  
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
 RA Pleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,  
 RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pasole G., Quackenbush J.,  
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,  
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
 RA Lyons P., Marchionni L., Maehina J., Mazzarelli J., Mombaerts P.,  
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,  
 RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,  
 RA Hayashizaki Y.;  
 RT "Functional annotation of a full-length mouse cDNA collection.";  
 RL Nature 409:685-690(2001).  
 RN [3]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J; TISSUE=Parthenogenote;  
 RX The FANTOM Consortium.  
 RA The RIKEN Genome Exploration Research Group Phase I & II Team;  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 60,770 full-length cDNAs.";  
 RL Nature 420:563-573(2002).  
 RN [4]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J; TISSUE=Parthenogenote;  
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;  
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,  
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;  
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to  
 prepare full-length cDNA libraries for rapid discovery of new genes.";  
 RL Genome Res. 10:1617-1630(2000).  
 RN [5]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J; TISSUE=Parthenogenote;  
 RX MEDLINE=20530913; PubMed=11076961; DOI=10.1101/gr.152600;  
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,  
 RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,  
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,  
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,  
 RA Fujiwaka S., Inoue K., Ogawa Y., Izawa M., Ohara E., Watahiki M.,  
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,  
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;  
 RT "RIKEN integrated sequence analysis (RISA) system-384-format  
 sequencing pipeline with 384 multicapillary sequencer.";  
 RL Genome Res. 10:1757-1771(2000).  
 RN [6]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J; TISSUE=Parthenogenote;  
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,  
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,  
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,  
 RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,  
 RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,  
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,  
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,

RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,  
 RA Sasaki D., Shibata K., Shingagawa A., Shiraki T., Sogabe Y., Tagami M.,  
 RA Tagawa A., Takahashi F., Takaku-Akaira S., Takeda Y., Tanaka T.,  
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;  
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
 CC 1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).  
 DR EMBL; AK045289; BAC32299.1; -, mRNA.  
 DR Ensembl; ENSMUSG00000049929; Mus musculus.  
 DR MGI; MGI:1925384; Gpr23.  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0045028; F:purinergic nucleotide receptor activity; G-. . .; IEA.  
 DR GO; GO:0004872; F:receptor activity; IEA.  
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.  
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.  
 DR GO; GO:0007165; P:signal transduction; IEA.  
 DR InterPro; IPR000276; GPCR Rhodopsn.  
 DR Pfam; PF00001; 7tm 1; 1.  
 DR PRINTS; PRO0237; GPCRHOPOPSN.  
 DR PROSITE; PRO1087; P2Y5ORPHAN.  
 DR PROSITE; PS00237; G PROTEIN RECP F1\_1; UNKNOWN 1.  
 DR PROSITE; PS0262; G PROTEIN RECP F1\_2; 1.  
 KW G-protein coupled receptor; Receptor; Transducer; Transmembrane.  
 SQ SEQUENCE 370 AA; 41872 MW; 084C79FEDFD32050 CRC64;  
 Query Match 24.2%; Score 391; DB 2; Length 370;  
 Best Local Similarity 34.5%; Pred. No. 3.1e-21;  
 Matches 97; Conservative 59; Mismatches 103; Indels 22; Gaps 9;  
 QY 25 AVIGLVLLVGLLLNSLALWVFCRMOQTETRYMTNLAVADLCILCTLP-VLHSLR-- 81  
 DB 44 AVYSVVFILITSSASLVFVCFRMMKSETAIFITNLALSLLVFCVTLPPFKIFYNFRH 103  
 QY 82 -DTSDTPLCOLSQGIYLTNRYSISLVTAIAVDYVAVRHPLRGLRSPRQAAAVCAVL 140  
 DB 104 WFFGDT-LCKISGTAFNLINIGSMLFLTCISVDRLAIVYPRSTIRTRNSAIVCAGV 162  
 QY 141 WVLVGTSLVARMLLQIQE-----GGPCPRSTRHNFNSMR--PPLIGFYPLAVVVF 189  
 DB 163 WLVLSGGGISASLFTSTTVNNATTTTCFEGFSKRVKTYLSKITITFIEVVGFIPLILNS 222  
 QY 190 CSLKVVYVTAALQRPPTDVGQAEAT-RKAKRMVWNLVVFVVCPLPLHVLGTVPLAVGNAC 248  
 DB 223 CSSVVLRITL--RKPAATLSQIGTNKKVKLVKMTVHMAVFCVCPVNSLVFLVALVRSQAI 280  
 QY 249 --ALLETIRRALY-ITSKLSANCCCLDAICYYYMAKEFQEA 286  
 DB 281 TNCLLERPAKIMYPITLCATLNCDFDPPIYYFTLESFQKS 321

Search completed: February 9, 2006, 01:00:18  
 Job time : 166.5 secs

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 9, 2006, 01:00:39 ; Search time 33.5 Seconds  
(without alignments)  
762.591 Million cell updates/sec

Title: US-10-083-168-85  
Perfect score: 1615  
Sequence: 1 MNGTYNTCGSSDLTWPPAIK.....AVAPRAKAHKSQDSLCVTLA 309

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: /cgn2\_6/ptodata/1/iaa/6 COMB.pep.\*  
3: /cgn2\_6/ptodata/1/iaa/H-COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/PCITUS COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/RE COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description        |
|------------|-------|-------------|--------|-------|--------------------|
| 1          | 1609  | 99.6        | 309    | 2     | US-09-422-869-20   |
| 2          | 401   | 24.8        | 370    | 2     | US-08-781-250-2    |
| 3          | 382.5 | 23.7        | 363    | 2     | US-10-314-048A-159 |
| 4          | 376.5 | 23.3        | 363    | 2     | US-10-314-048A-36  |
| 5          | 374.5 | 23.2        | 387    | 2     | US-09-170-496D-222 |
| 6          | 369.5 | 22.9        | 387    | 2     | US-09-170-496D-108 |
| 7          | 369.5 | 22.9        | 387    | 2     | US-09-944-807-21   |
| 8          | 369.5 | 22.9        | 387    | 2     | US-10-314-048A-135 |
| 9          | 360.5 | 22.3        | 344    | 1     | US-08-467-948A-8   |
| 10         | 360.5 | 22.3        | 344    | 2     | US-08-467-947A-8   |
| 11         | 360   | 22.3        | 372    | 2     | US-09-875-076-4    |
| 12         | 359.5 | 22.3        | 302    | 1     | US-08-467-948A-30  |
| 13         | 359.5 | 22.3        | 302    | 2     | US-08-467-947A-30  |
| 14         | 348.5 | 21.6        | 360    | 2     | US-10-314-048A-137 |
| 15         | 340.5 | 21.1        | 351    | 2     | US-10-314-048A-157 |
| 16         | 340   | 21.1        | 361    | 2     | US-10-314-048A-139 |
| 17         | 329.5 | 20.4        | 254    | 2     | US-09-964-956-83   |
| 18         | 328.5 | 20.3        | 377    | 2     | US-09-745-842-17   |
| 19         | 327.5 | 20.3        | 374    | 2     | US-09-102-710B-3   |
| 20         | 326   | 20.2        | 346    | 2     | US-10-314-048A-24  |
| 21         | 323.5 | 20.0        | 346    | 2     | US-10-314-048A-88  |
| 22         | 321.5 | 19.9        | 345    | 2     | US-09-979-603-18   |
| 23         | 320   | 19.8        | 362    | 2     | US-08-513-974B-374 |
| 24         | 319.5 | 19.8        | 343    | 2     | US-10-314-048A-151 |
| 25         | 318.5 | 19.7        | 346    | 2     | US-09-585-876-2    |
| 26         | 317.5 | 19.7        | 391    | 2     | US-09-826-509-463  |
| 27         | 316.5 | 19.6        | 346    | 2     | US-09-979-603-2    |

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|----|-------|------|-----|---|--------------------|-------------------|
| 28 | 316.5 | 19.6 | 346 | 2 | US-10-314-048A-14  | Sequence 14, Appl |
| 29 | 316   | 19.6 | 309 | 2 | US-09-979-603-22   | Sequence 22, Appl |
| 30 | 316   | 19.6 | 374 | 2 | US-09-745-842-15   | Sequence 15, Appl |
| 31 | 315.5 | 19.5 | 365 | 2 | US-09-745-842-16   | Sequence 16, Appl |
| 32 | 315.5 | 19.5 | 365 | 2 | US-09-077-173D-2   | Sequence 2, Appli |
| 33 | 315   | 19.5 | 373 | 2 | US-08-513-974B-373 | Sequence 173, App |
| 34 | 311.5 | 19.3 | 354 | 2 | US-09-364-425B-60  | Sequence 60, Appl |
| 35 | 311.5 | 19.3 | 362 | 2 | US-09-170-496D-4   | Sequence 4, Appli |
| 36 | 311.5 | 19.3 | 362 | 2 | US-09-850-948-2    | Sequence 2, Appli |
| 37 | 311.5 | 19.3 | 364 | 2 | US-08-148-708-2    | Sequence 186, App |
| 38 | 310.5 | 19.2 | 358 | 2 | US-09-170-496D-186 | Sequence 555, App |
| 39 | 310   | 19.2 | 342 | 2 | US-09-826-509-555  | Sequence 9, Appli |
| 40 | 309   | 19.1 | 342 | 2 | US-08-988-876-9    | Sequence 166, App |
| 41 | 307.5 | 19.0 | 362 | 2 | US-09-170-496D-166 | Sequence 2, Appli |
| 42 | 306.5 | 19.0 | 375 | 1 | US-08-442-134A-2   | Sequence 2, Appli |
| 43 | 306.5 | 19.0 | 375 | 1 | US-08-444-581B-2   | Sequence 2, Appli |
| 44 | 306.5 | 19.0 | 375 | 1 | US-08-446-088A-2   | Sequence 2, Appli |
| 45 | 306.5 | 19.0 | 375 | 1 | US-08-559-524A-3   | Sequence 3, Appli |

ALIGNMENTS

RESULT 1

US-09-422-869-20  
; Sequence 20, Application US/09422869  
; Patent No. 6235481  
; GENERAL INFORMATION:  
; APPLICANT: POLONSKI, KENNETH S.  
; APPLICANT: HORIKAWA, YUKIO  
; APPLICANT: ODA, NAOHISA  
; APPLICANT: COX, NANCY J.  
; APPLICANT: SEENAN, SEAMUS  
; APPLICANT: ZHOU, YUN-PING  
; APPLICANT: OTANI, KENICHI  
; APPLICANT: HANIS, CRAIG L.  
; APPLICANT: BELL, GRAEME I.  
; TITLE OF INVENTION: METHODS OF TREATMENT OF TYPE 2 DIABETES  
; FILE REFERENCE: ARCD:307  
; CURRENT APPLICATION NUMBER: US/09/422,869  
; CURRENT FILING DATE: 1999-10-21  
; EARLIER APPLICATION NUMBER: 60/134,175  
; EARLIER FILING DATE: 1999-05-13  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 20  
; LENGTH: 309  
; TYPE: PRT  
; ORGANISM: Human  
US-09-422-869-20

Query Match 99.6%; Score 1609; DB 2; Length 309;

Best Local Similarity 99.7%; Pred. No. 8.1e-132; Indels 0; Gaps 0;  
Matches 308; Conservative 0; Mismatches 1;

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| Db | 1   | MNGTYNTCGSSDLTWPPAIKLGFGVAYLGVLLVLGLLNSLALWVFCRMOQWTETRIYMT | 60  |
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| Qy | 121 | PLRARGLRSPQAAAVCAVLWLVIGSLVAVRWLIGQGGCFRSTRNFNSMRPPLIGF     | 180 |
| Db | 121 | PLRARGLRSPQAAAVCAVLWLVIGSLVAVRWLIGQGGCFRSTRNFNSMRPPLIGF     | 180 |
| Qy | 181 | YLPLAVVFCSLKVVTALAQRPPTDVGQAEATRAKRWANLLVVFVVCFLPLHVLTVR    | 240 |
| Db | 181 | YLPLAVVFCSLKVVTALAQRPPTDVGQAEATRAKRWANLLVVFVVCFLPLHVLTVR    | 240 |
| Qy | 241 | LAVGNACALLETIRRALYITSKLSDANCCCLDAICYYTMAKEFOEASALAVAPRAKAHS | 300 |
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Db 264 QNCEVRSVDLAFFITLSFTYNSMLDPVYYFSSPSF 301

## RESULT 4

US-10-314-048A-36  
; Sequence 36, Application US/10314048A

; Patent No. 6902902

## GENERAL INFORMATION:

; APPLICANT: Unett, David J.

; APPLICANT: Chen, Ruoping

; APPLICANT: Richman, Jeremy

; APPLICANT: Connolly, Daniel

; APPLICANT: Dang, Huong T.

; APPLICANT: Choi, Bryan

; APPLICANT: Leonard, James

; APPLICANT: Hakak, Yaron

; APPLICANT: Liaw, Chen

; APPLICANT: Lowitz, Kevin P.

; APPLICANT: Behan, Dominic P.

; APPLICANT: Chalmers, Derek T.

; APPLICANT: Lerner, Michael

; TITLE OF INVENTION: Human G Protein-Coupled Receptors and Modulators Thereof

; FILE REFERENCE: 22 US6.CIP

; CURRENT APPLICATION NUMBER: US/10/314,048A

; CURRENT FILING DATE: 2002-12-06

; PRIOR APPLICATION NUMBER: 10/096,511

; PRIOR FILING DATE: 2002-03-12

; PRIOR APPLICATION NUMBER: 09/995,543

; PRIOR FILING DATE: 2001-11-27

; PRIOR APPLICATION NUMBER: 60/399,917

; PRIOR FILING DATE: 2002-07-29

; PRIOR APPLICATION NUMBER: 60/404,761

; PRIOR FILING DATE: 2002-08-19

; PRIOR APPLICATION NUMBER: 60/410,747

; PRIOR FILING DATE: 2002-09-13

; NUMBER OF SEQ ID NOS: 161

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 36

; LENGTH: 363

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-314-048A-36

Query Match 23.3%; Score 376.5; DB 2; Length 363;

Best Local Similarity 34.8%; Pred. No. 6.3e-25;

Matches 97; Conservative 45; Mismatches 104; Indels 33; Gaps 11;

Qy 27 LGVLLVGLLNSLALWVFCRCMQWTETRIYMTNLAVADCLLCTLPFVLHSL-----R 81

Db 34 LGLEFIFGLLNGLALWIFCFHLKSWKSSRIFLNFNLAVADFLIICLPFVMDYVRRSDW 93

Qy 82 DTSPTPLCQLSQGIYLTNRNYSISLVTAIAVDYVAVRHPLRARGLRSPROAAAVCAVLW 141

Db 94 KFGDIP-CLMLFPLMNRQCSIIFLTVAVDYVFRVVPHPHALNKNISNWTAAIISCLW 152

Qy 142 VLVIGSLV--ARWLGIOEGG--FCFR-STRHNF--NSMRPPLGLFYPLAVVVFCSLKV 194

Db 153 GITIGLTVHLKKKKPIQNGGANLCSFSICHTFQWHEAMF-LLEFFLPLGLIILFCSARI 211

Qy 195 VTALAQRPTDVGQAEATKAKR-----MWNALLVFWVCFPLPHVGLTVRLAVGW----- 245

Db 212 IWSLQR-----QMDRHAKIKRAITFMVVAIVFVICFLP---SVVVRIRIFWLLHTSG 262

Qy 246 -NACALLTIRRALYITSKLSANCCCLDAICYYYMAKEF 283

Db 263 TQNCVRSVDLAFFITLSFTYNSMLDPVYYFSSPSF 301

## RESULT 5

US-09-170-496D-222

; Sequence 222, Application US/09170496D

; Patent No. 6555339

## GENERAL INFORMATION:

; APPLICANT: Behan, Dominic P.

; APPLICANT: Chalmers, Derek T.

; APPLICANT: Liaw, Chen W.

; TITLE OF INVENTION: Receptors

; FILE REFERENCE: AREN-0040

; CURRENT APPLICATION NUMBER: US/09/170,496D

; CURRENT FILING DATE: 1998-10-13

; NUMBER OF SEQ ID NOS: 294

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 222

; LENGTH: 387

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-170-496D-222

Query Match 23.2%; Score 374.5; DB 2; Length 387;

Best Local Similarity 34.4%; Pred. No. 1e-24;

Matches 95; Conservative 47; Mismatches 107; Indels 27; Gaps 10;

Qy 27 LGVLLVGLLNSLALWVFCRCMQWTETRIYMTNLAVADCLLCTLPFVLHSLRDTSDT 86

Db 34 LGLEFIFGLLNGLALWIFCFHLKSWKSSRIFLNFNLAVADFLIICLPFVMDYVRRSDW 93

Qy 87 PL-----COLSQGIYLTNRNYSISLVTAIAVDYVAVRHPLRARGLRSPROAAAVCAVLW 142

Db 94 KFGDIP-CLRLVFLPMNRQCSIIFLTVAVDYVFRVVPHPHALNKNISNWTAAIISCLW 153

Qy 143 LVIG---SLVARWLGIOEG--GFCFR-STRHNF--NSMRPPLGLFYPLAVVVFCSLKV 194

Db 154 ITVGLTVHLKKKLL-IQNGPANVCISFSICHTFRWHEAMF-LLEFFLPLGLIILFCSARI 211

Qy 195 VTALAQRPTDVGQAEATKAKRWNANLAVFVVCFLPHVGLTVRLAVGW-----NA 247

Db 212 IWSLQR---QMDRHAKIKRAITFMVVAIVFVICFLP---SVVVRIRIFWLLHTSGTON 265

Qy 248 CALLETIRRALYITSKLSANCCCLDAICYYYMAKEF 283

Db 266 CEVRSVDLAFFITLSFTYNSMLDPVYYFSSPSF 301

## RESULT 6

US-09-170-496D-108

; Sequence 108, Application US/09170496D

; Patent No. 6555339

## GENERAL INFORMATION:

; APPLICANT: Behan, Dominic P.

; APPLICANT: Chalmers, Derek T.

; APPLICANT: Liaw, Chen W.

; TITLE OF INVENTION: Receptors

; FILE REFERENCE: AREN-0040

; CURRENT APPLICATION NUMBER: US/09/170,496D

; CURRENT FILING DATE: 1998-10-13

; NUMBER OF SEQ ID NOS: 294

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 108

; LENGTH: 387

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-170-496D-108

Query Match 22.9%; Score 369.5; DB 2; Length 387;

Best Local Similarity 35.0%; Pred. No. 2.7e-24;

Matches 98; Conservative 45; Mismatches 102; Indels 35; Gaps 12;

Qy 27 LGVLLVGLLNSLALWVFCRCMQWTETRIYMTNLAVADCLLCTLPFVL-----HSILR 81

Db 34 LGLEFIFGLLNGLALWIFCFHLKSWKSSRIFLNFNLAVADFLIICLPFVMDYVRRSDW 93

Qy 82 DTSPTPLCQLSQGIYLTNRNYSISLVTAIAVDYVAVRHPLRARGLRSPROAAAVCAVLW 141





CITY: WASHINGTON  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY DISK  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/467,948A  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/04079  
FILING DATE: 30-MAR-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: STEFFE, ERIC K.  
REGISTRATION NUMBER: 36,698  
REFERENCE/DOCKET NUMBER: 1488.1140003/EKS/KLM  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-2600  
TELEFAX: 202-371-2540  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 344 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-467-948A-8

|                       |       |  |         |            |        |        |    |      |    |
|-----------------------|-------|--|---------|------------|--------|--------|----|------|----|
| Query Match           | 22.3% | Score  | 360.5   | DB 1       | Length | 344    |    |      |    |
| Best Local Similarity | 29.2% | Pred. NO.  | 1.4e-23 |            |        |        |    |      |    |
| Matches               | 90    | Conservative   | 68      | Mismatches | 107    | Indels | 43 | Gaps | 10 |
| QY                    | 10    | SSDLTPPAIKLGFAYVL-GVLLVLGLLLNSLALWVFCRMMQQTETRIYMTNLAVADLC     | 68      |            |        |        |    |      |    |
| Db                    | 6     | SSHCFYNDSPFKYLYGCMFPMVFLGLISNCVAIYFICVLKVRNETTYMINLAMSLL       | 65      |            |        |        |    |      |    |
| QY                    | 69    | LLCTLPLVHLSRDTSDTP-----LCQLSQIGYLYLNRMYMSISLVTAIAVDRXAVVRHPLRA | 124     |            |        |        |    |      |    |
| Db                    | 66    | FVETLPPRIIFYF-TTRNPPFGDLLCKISVMLFYTNMYGSIILFLTCSVDRELAIVYPPKS  | 124     |            |        |        |    |      |    |
| QY                    | 125   | RGLRSPPROAAVCAVLVLVI-GSLVARWLIGIQEG-----FCFSTRHFNPSMRPP--      | 176     |            |        |        |    |      |    |
| Db                    | 125   | KTLRTKRNAKIVCTGWMLTVIGGSAFVFGVOSTHSQGNNASEACFEN-----PPEA       | 175     |            |        |        |    |      |    |
| QY                    | 177   | -----LLGFVLPLAVVFCSLKVVTALAQRPPTDVGQAATR-KAKRMVWA              | 221     |            |        |        |    |      |    |
| Db                    | 176   | TWKTVLSRIVFIEIVGFPFIPULMNTCSSWLKLTLC--PVTLSRSKINKTKVLMIFV      | 233     |            |        |        |    |      |    |
| QY                    | 222   | NLLVFWVCFLPHVGLTVRLAVGNA--CALLETIRRALYITSKLSDANCCLDAICYYY      | 278     |            |        |        |    |      |    |
| Db                    | 234   | HLIIFCFEVPYNNILYSLVRTQTFVNCVSVAAVRTMYPIITLCIAVSNCCFDIVVYF      | 293     |            |        |        |    |      |    |
| QY                    | 279   | MAKEFOEA   | 286     |            |        |        |    |      |    |
| Db                    | 294   | TSDTIONS   | 301     |            |        |        |    |      |    |

RESULT 10  
US-08-467-947A-8  
/ Sequence 8, Application US/08467947A  
/ Patent No. 6090575  
/ GENERAL INFORMATION:  
/ APPLICANT: LI, YI  
/ APPLICANT: CAO, LIANG  
/ APPLICANT: NI, JIAN  
/ APPLICANT: GENTZ, REINER  
/ APPLICANT: BULT, CAROL J.  
/ APPLICANT: SUTTON III, GRANGER G  
/ APPLICANT: ROSEN, CRAIG A.  
/ TITLE OF INVENTION: Polyfunctional

; TITLE OF INVENTION: Coupled Receptor GPR1  
 ; NUMBER OF SEQUENCES: 30  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
 ; STREET: 1100 NEW YORK AVE., NW, SUITE 600  
 ; CITY: WASHINGTON  
 ; STATE: DC  
 ; COUNTRY: USA  
 ; ZIP: 20005  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: FLOPPY DISK  
 ; COMPUTER: IBM PC COMPATIBLE  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/467,947A  
 ; FILING DATE: 06-JUN-1995  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: PCT/US95/04079  
 ; FILING DATE: 30-MAR-1995  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: STEFFE, ERIC K.  
 ; REGISTRATION NUMBER: 36,688  
 ; REFERENCE/DOCKET NUMBER: 1488.1140002/EKS/KLM  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 202-371-2600  
 ; TELEFAX: 202-371-2540  
 ; INFORMATION FOR SEQ ID NO: 8:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 344 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-08-467-947A-8

|                       |       |  |         |            |        |        |    |      |    |
|-----------------------|-------|--|---------|------------|--------|--------|----|------|----|
| Query Match           | 22.3% | Score  | 360.5   | DB 2       | Length | 344    |    |      |    |
| Best Local Similarity | 29.2% | Pred. No.  | 1.4e-23 |            |        |        |    |      |    |
| Matches               | 90    | Conservative   | 68      | Mismatches | 107    | Indels | 43 | Gaps | 10 |
| Qy                    | 10    | SSDLTPPAIKLGFVAYL-VGLLVGLLLNSLALWVFCRQMOWTETRIYMTNLAVADLC      | 68      |            |        |        |    |      |    |
| Db                    | 6     | SSHCFYNDSEFKYTYGCMFWMVFLVGLISNCVAIYIFCVLKVRNETTYMINLAMSDDL     | 65      |            |        |        |    |      |    |
| Qy                    | 69    | LLCTLPFLVHSLRDTSDTP-----LCQLSQIGIYLTNRNYSISLVTAIAVDRVAVVRHPLRA | 124     |            |        |        |    |      |    |
| Db                    | 66    | FVFTLPFRIFPYF-TTRNWPFGDLLCKISVWMLFYTNMYGSSILFLTCISVDRLAIVYPEKS | 124     |            |        |        |    |      |    |
| Qy                    | 125   | RGLRSPPQAAACVAVLVVI-GSLVARWLLGIOEGG-----FCFSTRHFNFSNRFP--      | 176     |            |        |        |    |      |    |
| Db                    | 125   | KTLRTKRNAKIVCTGVMLTVIGGSAPAFVQSTHSQGNNASEACFEN-----FPEA        | 175     |            |        |        |    |      |    |
| Qy                    | 177   | -----LLGPLYPLAVVFCGLKVVTALAQRPPTDVGQAEATR-KAKRMVWA             | 221     |            |        |        |    |      |    |
| Db                    | 176   | TWKTYLSRIVIFIEIVGFFIPLINVTCSMWLKITLK--PVYLSRSKINKTKVLKMLFV     | 233     |            |        |        |    |      |    |
| Qy                    | 222   | NLLVFWVCFLPLRVGLTVRLAVGWNA---CALLETTRREALYITSKLSDANCCCLDAICYY  | 278     |            |        |        |    |      |    |
| Db                    | 234   | HLIIFCFCEVPYNILYLSVRTQTFVNCVSVAAVRTWYPIITLCIAVSNCCFPDVIYYV     | 293     |            |        |        |    |      |    |
| Qy                    | 279   | MAKBFQEA   | 286     |            |        |        |    |      |    |
| Db                    | 294   | TSDTIQNS   | 301     |            |        |        |    |      |    |

RESULT 11  
US-09-875-076-4  
; Sequence 4, Application US/09875076  
; Patent No. 6869776  
; GENERAL INFORMATION:  
; APPLICANT: Chen, Ruoping  
; APPLICANT: Dang, Huong T.  
; APPLICANT: Liaw, Chen W.

APPLICANT: Lin, I-Lin  
TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors

FILE REFERENCE: AREN0050

CURRENT APPLICATION NUMBER: US/09/875,076

CURRENT FILING DATE: 2001-06-06

PRIOR APPLICATION NUMBER: 09/417,044

PRIOR FILING DATE: 1999-10-12

PRIOR APPLICATION NUMBER: 60/120,416

PRIOR FILING DATE: 1999-02-16

PRIOR APPLICATION NUMBER: 60/121,851

PRIOR FILING DATE: 1999-02-26

PRIOR APPLICATION NUMBER: 60/123,946

PRIOR FILING DATE: 1999-03-12

PRIOR APPLICATION NUMBER: 60/123,949

PRIOR FILING DATE: 1999-03-12

PRIOR APPLICATION NUMBER: 60/136,436

PRIOR FILING DATE: 1999-05-28

PRIOR APPLICATION NUMBER: 60/136,437

PRIOR FILING DATE: 1999-05-28

PRIOR APPLICATION NUMBER: 60/136,439

PRIOR FILING DATE: 1999-05-28

PRIOR APPLICATION NUMBER: 60/136,567

PRIOR FILING DATE: 1999-05-28

PRIOR APPLICATION NUMBER: 60/137,127

PRIOR FILING DATE: 1999-05-28

PRIOR APPLICATION NUMBER: 60/137,131

PRIOR FILING DATE: 1999-05-28

PRIOR APPLICATION NUMBER: 60/141,448

PRIOR FILING DATE: 1999-06-29

PRIOR APPLICATION NUMBER: 60/156,653

PRIOR FILING DATE: 1999-09-29

PRIOR APPLICATION NUMBER: 60/156,633

PRIOR FILING DATE: 1999-09-29

PRIOR APPLICATION NUMBER: 60/156,555

PRIOR FILING DATE: 1999-09-29

PRIOR APPLICATION NUMBER: 60/156,634

PRIOR FILING DATE: 1999-09-29

PRIOR APPLICATION NUMBER: 60/157,280

PRIOR FILING DATE: 1999-10-01

PRIOR APPLICATION NUMBER: 60/157,294

PRIOR FILING DATE: 1999-10-01

PRIOR APPLICATION NUMBER: 60/157,281

PRIOR FILING DATE: 1999-10-01

PRIOR APPLICATION NUMBER: 60/157,293

PRIOR FILING DATE: 1999-10-01

PRIOR APPLICATION NUMBER: 60/157,282

PRIOR FILING DATE: 1999-10-01

NUMBER OF SEQ ID NOS: 74

SOFTWARE: Patent In Ver. 2.1

SEQ ID NO 4

LENGTH: 372

TYPE: PRT

ORGANISM: Homo sapiens

US-09-875-076-4

Query Match 22.3%; Score 360; DB 2; Length 372;

Best Local Similarity 33.7%; Pred. No. 1.7e-23;

Matches 109; Conservative 47; Mismatches 125; Indels 42; Gaps 12;

QY 6 NTGSGDLTWP---PAIKGFYAYLGVLVLGLLNSLALWVFCRMOQWETRIYNTYL 62

Db 6 SSTNSVLPCPDYRPHRTLHLVY-SLVLAAGLPLNALWFLRALRVHSVVVMCNL 64

QY 63 AVADLCLCTLP-----FVLHSLRSDTDP-----LCQLSQGIYLTNRYSISLVTAIYD 113

Db 65 RASDLLPTLSLPVRLSYALH-----HWFPDLLCQTTCGAFQNMVYSCIFLMLIND 118

QY 114 RVAVRHPLRAGLRSPQAAVCAVLWVLVTGSLV-----ARWLIGIOGGCFPS 165

Db 119 RYAAIVHPLRLHLRRPRVARLLCLGVWALILVFAVPAARVHRPSRCRVDLVRVLCFS 178

QY 166 -TRHFNNSRFP-----LGFVLPLAVVFCSLKVVTLAQRPPDVCQAETRAKEM 218

Db 179 FSDLMKGRLLPLVLLAEALGFLLPLAAVVYSSGRVFWTLA-RP--DATSQRRRTVRL 235

QY 219 VMANLVFVVCFLPHVGLTV----RLAVGMNACALLETIRRALYITTSKLSANCCLDAL 274

Db 236 LLANLVIFLLCFVYNSTLAVYGLLRSLKVAASVPARDVRGVLMVMVLLAGANCVDPL 295

QY 275 CYYMAKEFOEA-SALAVAPRAK 296

Db 296 VYFSAAGFRNTLRGLGTPHRAK 318

# RESULT 12

US-08-467-948A-30

Sequence 30, Application US/08467948A

Patent No. 5998164

GENERAL INFORMATION:

APPLICANT: LI, YI

APPLICANT: CAO, LIANG

APPLICANT: NI, JIAN

APPLICANT: GENTZ, REINER

APPLICANT: BULT, CAROL J.

APPLICANT: SUTTON III, GRANGER G.

APPLICANT: ROSEN, CRAIG A.

TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein

TITLE OF INVENTION: Coupled Receptor GPR2

NUMBER OF SEQUENCES: 30

CORRESPONDENCE ADDRESS:

ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.

STREET: 1100 NEW YORK AVE., NW, SUITE 600

CITY: WASHINGTON

STATE: DC

COUNTRY: USA

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/467,948A

FILING DATE: 06-JUN-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/04079

FILING DATE: 30-MAR-1995

ATTORNEY/AGENT INFORMATION:

NAME: STEFFE, ERIC K.

REGISTRATION NUMBER: 36,688

REFERENCE/DOCKET NUMBER: 1488.1140003/EKS/KLM

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-371-2600

TELEFAX: 202-371-2540

INFORMATION FOR SEQ ID NO: 30:

SEQUENCE CHARACTERISTICS:

LENGTH: 302 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: not relevant

MOLECULE TYPE: peptide

US-08-467-948A-30

Query Match 22.3%; Score 359.5; DB 1; Length 302;

Best Local Similarity 30.0%; Pred. No. 1.5e-23;

Matches 90; Conservative 64; Mismatches 103; Indels 43; Gaps 10;

QY 10 SSDLTWPAIKLGFY-AYLGVLVLGLLNSLALWVFCRMOQWETRIYNTNLAVADLC 68

Db 1 SSNCSTEDSFKTYLGCVFMSVFLGLANCVAIYFTFLKVRNETTTTMLMLAISDLL 60

QY 69 LCLTLPFVLHSLRSDTDP-----LCQLSQGIYLTNRYSISLVTAIYDVRVVRHPLRA 124

Db 61 FVFTLIPFRIIYF-VVRNWPFGDVLCKISVTLPTNNYGSILFCLTCLISVDRLAIVHPPRS 119



Db 210 WSLRQR-----QMDRHAKIKRAINFIMVVAIVFIICFLP---SVAVRIRFWLLKYKNV 260  
QY 246 NACALLETRRRLYITSKLSNDANCCLDCAICYTMAKEP 283  
Db 261 RNCDIYSSVDLAFFTLTSLTYNNSMLDPVVYFSSPSF 298

RESULT 15

US-10-314-048A-157  
; Sequence 157, Application US/10314048A  
; Patent No. 6902902  
; GENERAL INFORMATION:  
; APPLICANT: Unett, David J.  
; APPLICANT: Chen, Ruoping  
; APPLICANT: Richman, Jeremy  
; APPLICANT: Connolly, Daniel  
; APPLICANT: Dang, Huong T.  
; APPLICANT: Choi, Bryan  
; APPLICANT: Leonard, James  
; APPLICANT: Hakak, Yaron  
; APPLICANT: Liaw, Chen  
; APPLICANT: Lowitz, Kevin P.  
; APPLICANT: Behan, Dominic P.  
; APPLICANT: Chalmers, Derek T.  
; APPLICANT: Lerner, Michael  
; TITLE OF INVENTION: Human G Protein-Coupled Receptors and Modulators Thereof  
; FILE REFERENCE: 22.US6.CIP  
; CURRENT APPLICATION NUMBER: US/10/314,048A  
; CURRENT FILING DATE: 2002-12-06  
; PRIOR APPLICATION NUMBER: 10/096,511  
; PRIOR FILING DATE: 2002-03-12  
; PRIOR APPLICATION NUMBER: 09/995,543  
; PRIOR FILING DATE: 2001-11-27  
; PRIOR APPLICATION NUMBER: 60/399,917  
; PRIOR FILING DATE: 2002-07-29  
; PRIOR APPLICATION NUMBER: 60/404,761  
; PRIOR FILING DATE: 2002-08-19  
; PRIOR APPLICATION NUMBER: 60/410,747  
; PRIOR FILING DATE: 2002-09-13  
; NUMBER OF SEQ ID NOS: 161  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 157  
; LENGTH: 351  
; TYPE: PRT  
; ORGANISM: Rat  
US-10-314-048A-157

Query Match 21.1%; Score 340.5; DB 2; Length 351;  
Best Local Similarity 33.2%; Pred. No. 8e-22;  
Matches 107; Conservative 48; Mismatches 114; Indels 53; Gaps 15;  
QY 16 PPAIKLGFYVLGVLLVGLLNSLALWVFCRCMQMTETRIYMTNLAVADLCCLTLPF 75  
Db 27 PELLILAF-----LLGALGNLALCGCFHMTKWSSTIYLFNLAVADFLLMICPL 78  
QY 76 -VLHSLRD---TSDFPLCQLSQGIYLTNRYSISLVTAIVDHYVAVRHPRLRGLRSP 130  
Db 79 RTDYLLRRRHILGDIP-CLVLFLMLANNRAGSIVPLTVVAVDRYFKVHPHMYNAISN 137  
QY 131 RQAAAVCAVLWVLVIGSLVARMVLGIQEGGCFR-----STRNFNSMRPPLIG 179  
Db 138 RTAAATVCLVTLVILGTV--YLL--MESHLCVRGMVSSCSFIMESANGWHDIMFQ-LE 192  
QY 180 FYLPLAVVVFCSIKVVTALAQRPPTDVQAEATRAKRMVMANLLVFVVCPLPLHGLTV 239  
Db 193 FFLPLTLILFCFKVWSLRQ--QQLTQARMRRATRFIMVVASVFITCILP----SVLA 247  
QY 240 RLAVGW---NACALLETRRRLYITSKLSNDANCCLDCAICYTMAKEPQEAASA----LAV 291  
Db 248 RLYFLWTPVSSACD--PSVHIALHVTLSLTYLNSMLDPLVYFSSPSPPKFKAKLIRSL 305

QY 292 AP-----RAKAHKSQD-----SLC 305  
Db 306 KPRRPGRSQARRSEMPISNLC 327  
Search completed: February 9, 2006, 01:02:28  
Job time : 34.5 secs

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 9, 2006, 01:16:44 ; Search time 118.5 Seconds  
(without alignments)  
1089.530 Million cell updates/sec

Title: US-10-083-168-85  
Perfect score: 1615  
Sequence: 1 MNGTYNTCGSSDLTWPPAIK.....AVAPRAKHKSDSLCVTLA 309

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA Main:  
1: /cgm2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*  
2: /cgm2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*  
3: /cgm2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep.\*  
4: /cgm2\_6/ptodata/1/pubpaa/US10\_PUBCOMB.pep.\*  
5: /cgm2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*  
6: /cgm2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description                          |
|------------|-------|-------------|--------|----|--------------------------------------|
| 1          | 1609  | 99.6        | 309    | 3  | US-09-768-877-20 Sequence 20, Appl   |
| 2          | 1609  | 99.6        | 309    | 4  | US-10-225-567A-492 Sequence 492, App |
| 3          | 1609  | 99.6        | 309    | 5  | US-10-696-639-44 Sequence 44, Appl   |
| 4          | 1603  | 99.3        | 547    | 5  | US-10-505-486-84 Sequence 84, Appl   |
| 5          | 1597  | 98.9        | 309    | 4  | US-10-157-031-351 Sequence 351, App  |
| 6          | 401   | 24.8        | 370    | 3  | US-09-964-821B-11 Sequence 11, Appl  |
| 7          | 401   | 24.8        | 370    | 4  | US-10-081-810-44 Sequence 44, Appl   |
| 8          | 401   | 24.8        | 370    | 4  | US-10-225-567A-225 Sequence 225, App |
| 9          | 401   | 24.8        | 370    | 4  | US-10-024-298A-176 Sequence 176, App |
| 10         | 401   | 24.8        | 370    | 4  | US-10-042-211A-176 Sequence 176, App |
| 11         | 401   | 24.8        | 370    | 4  | US-10-268-332-11 Sequence 11, Appl   |
| 12         | 401   | 24.8        | 370    | 4  | US-10-617-217A-176 Sequence 176, App |
| 13         | 401   | 24.8        | 370    | 4  | US-10-775-965-11 Sequence 11, Appl   |
| 14         | 401   | 24.8        | 370    | 4  | US-10-024-298A-176 Sequence 176, App |
| 15         | 401   | 24.8        | 370    | 5  | US-10-753-267-86 Sequence 86, Appl   |
| 16         | 401   | 24.8        | 608    | 5  | US-10-505-486-114 Sequence 114, App  |
| 17         | 400   | 24.8        | 370    | 3  | US-09-964-821B-10 Sequence 10, Appl  |
| 18         | 400   | 24.8        | 370    | 4  | US-10-268-332-10 Sequence 10, Appl   |
| 19         | 391   | 24.2        | 370    | 4  | US-10-024-298A-174 Sequence 174, App |
| 20         | 391   | 24.2        | 370    | 4  | US-10-042-211A-174 Sequence 174, App |
| 21         | 391   | 24.2        | 370    | 4  | US-10-617-217A-174 Sequence 174, App |
| 22         | 391   | 24.2        | 370    | 4  | US-10-024-298A-174 Sequence 174, App |
| 23         | 389   | 24.1        | 368    | 4  | US-10-775-965-10 Sequence 10, Appl   |
| 24         | 382.5 | 23.7        | 363    | 4  | US-10-314-048A-159 Sequence 159, App |
| 25         | 382.5 | 23.7        | 363    | 5  | US-10-897-815-159 Sequence 159, App  |
| 26         | 382.5 | 23.7        | 363    | 5  | US-10-930-662-159 Sequence 159, App  |
| 27         | 377.5 | 23.4        | 363    | 3  | US-09-930-334-16 Sequence 16, Appl   |

ALIGNMENTS

RESULT 1

US-09-768-877-20  
; Sequence 20, Application US/09768877  
; Patent No. US20020150896A1  
; GENERAL INFORMATION:

; APPLICANT: POLONSKI, KENNETH S.  
; APPLICANT: HORIKAWA, YUKIO  
; APPLICANT: ODA, NAOHISA  
; APPLICANT: COX, NANCY J.  
; APPLICANT: SREENAN, SEAMUS  
; APPLICANT: ZHOU, YUN-PING  
; APPLICANT: OTANI, KENICHI  
; APPLICANT: HANIS, CRAIG I.  
; APPLICANT: BELL, GRAEME I.

; TITLE OF INVENTION: METHODS OF TREATMENT OF TYPE 2 DIABETES

; FILE REFERENCE: ARCD:307

; CURRENT APPLICATION NUMBER: US/09/768,877

; CURRENT FILING DATE: 2001-01-23

; PRIOR APPLICATION NUMBER: 09/422,869

; PRIOR FILING DATE: 1999-10-21

; NUMBER OF SEQ ID NOS: 30

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 20

; LENGTH: 309

; TYPE: PRT

; ORGANISM: Human

US-09-768-877-20

Query Match 99.6%; Score 1609; DB 3; Length 309;

Best Local Similarity 99.7%; Pred. No. 6.9e-147; Indels 0; Gaps 0;

Matches 308; Conservative 0; Mismatches 1;

Qy 1 MNGTYNTCGSSDLTWPPAIKLGFGYAYLGLVLGLLNSLALWVFCRCMQQTETRIYMT 60

Db 1 MNGTYNTCGSSDLTWPPAIKLGFGYAYLGLVLGLLNSLALWVFCRCMQQTETRIYMT 60

Qy 61 NLAVADLCLLCTLPFVLHSLRSDTDPQLCSQGIYLTNRVMSISLVTIAVDRVAVRH 120

Db 61 NLAVADLCLLCTLPFVLHSLRSDTDPQLCSQGIYLTNRVMSISLVTIAVDRVAVRH 120

Qy 121 PLRAGLSPQAAAVCAVLWLVIGSLVARWLLGIQGGCFSTRNENSMRPLLCGF 180

Db 121 PLRAGLSPQAAAVCAVLWLVIGSLVARWLLGIQGGCFSTRNENSMRPLLCGF 180

Qy 181 YLPLAVVVFCSLKVVTTALAQRPTDVQAEATRAKRWVWNLVVFVCFPLPHVGLTVR 240

Db 181 YLPLAVVVFCSLKVVTTALAQRPTDVQAEATRAKRWVWNLVVFVCFPLPHVGLTVR 240

Qy 241 LAVGWNACALLETTRRALYITSKLSDANCCLDALCIYYYNMAKEFQASALAVAPRAKHK 300

Db 241 LAVGWNACALLETTRRALYITSKLSDANCCLDALCIYYYNMAKEFQASALAVAPRAKHK 300

Db 241 LAVGNACALLETIRRALYITSLKSDANCCCLDAICYYMAKEFQBSALAVAPRAKAHKS 300  
QY 301 QDSLVCVTLA 309  
Db 301 QDSLVCVTLA 309

## RESULT 2

US-10-225-567A-492  
; Sequence 492, Application US/10225567A  
; Publication No. US20030113798A1  
; GENERAL INFORMATION:  
; APPLICANT: LifeSpan BioSciences  
; APPLICANT: Brown, Joseph P.  
; APPLICANT: Bourner, Maureen J.  
; APPLICANT: Roush, Christine L.  
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS  
; FILE REFERENCE: 1920-4-4  
; CURRENT FILING DATE: 2001-12-19  
; PRIOR APPLICATION NUMBER: US/10/225,567A  
; PRIOR FILING DATE: 2001-12-19  
; PRIOR FILING DATE: 2000-12-19  
; NUMBER OF SEQ ID NOS: 2292  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 492  
; LENGTH: 309  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-225-567A-492

Query Match 99.6%; Score 1609; DB 4; Length 309;  
Best Local Similarity 99.7%; Pred. No. 6.9e-147;  
Matches 308; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNGTYNTCGSSDLTPWPPAIKLGFYAYLGVLVLLGLLNSLALWVFCRMOQWTETRIYMT 60  
Db 1 MNGTYNTCGSSDLTPWPPAIKLGFYAYLGVLVLLGLLNSLALWVFCRMOQWTETRIYMT 60  
QY 61 NLAVADCLLCTLPFVLSLRDTSPTPLCQLSQGIYLTNRYSISLVTIAVDRYVAVRH 120  
Db 61 NLAVADCLLCTLPFVLSLRDTSPTPLCQLSQGIYLTNRYSISLVTIAVDRYVAVRH 120  
QY 121 PLRARGLSRPROAAVCAVLMVLVIGSLVARWLLGIQEGGFCFRSTRHFNFSMRPPLIGF 180  
Db 121 PLRARGLSRPROAAVCAVLMVLVIGSLVARWLLGIQEGGFCFRSTRHFNFSMRPPLIGF 180  
QY 181 YLPLAVVVFCSLKVVTAQAQPPTDVGOAEATRKAKRMVWNLVVFVCFPLPHVGLTVR 240  
Db 181 YLPLAVVVFCSLKVVTAQAQPPTDVGOAEATRKAKRMVWNLVVFVCFPLPHVGLTVR 240  
QY 241 LAVGNACALLETIRRALYITSLKSDANCCCLDAICYYMAKEFQBSALAVAPRAKAHKS 300  
Db 241 LAVGNACALLETIRRALYITSLKSDANCCCLDAICYYMAKEFQBSALAVAPRAKAHKS 300  
QY 301 QDSLVCVTLA 309  
Db 301 QDSLVCVTLA 309

## RESULT 3

US-10-696-639-44  
; Sequence 44, Application US/10696639  
; Publication No. US20050037439A1  
; GENERAL INFORMATION:  
; APPLICANT: Pharmacia Corporation  
; APPLICANT: Bourner, Maureen J.  
; TITLE OF INVENTION: DIFFERENTIALLY EXPRESSED GENES INVOLVED IN CANCER, THE  
; FILE REFERENCE: 01040/1  
; CURRENT APPLICATION NUMBER: US/10/696,639  
; CURRENT FILING DATE: 2003-10-29  
; PRIOR APPLICATION NUMBER: 60/422,176  
; PRIOR FILING DATE: 2002-10-29

; NUMBER OF SEQ ID NOS: 3114  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 44  
; LENGTH: 309  
; TYPE: PRT  
; ORGANISM: homo sapiens  
US-10-696-639-44

Query Match 99.6%; Score 1609; DB 5; Length 309;  
Best Local Similarity 99.7%; Pred. No. 6.9e-147;  
Matches 308; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNGTYNTCGSSDLTPWPPAIKLGFYAYLGVLVLLGLLNSLALWVFCRMOQWTETRIYMT 60  
Db 1 MNGTYNTCGSSDLTPWPPAIKLGFYAYLGVLVLLGLLNSLALWVFCRMOQWTETRIYMT 60  
QY 61 NLAVADCLLCTLPFVLSLRDTSPTPLCQLSQGIYLTNRYSISLVTIAVDRYVAVRH 120  
Db 61 NLAVADCLLCTLPFVLSLRDTSPTPLCQLSQGIYLTNRYSISLVTIAVDRYVAVRH 120  
QY 121 PLRARGLSRPROAAVCAVLMVLVIGSLVARWLLGIQEGGFCFRSTRHFNFSMRPPLIGF 180  
Db 121 PLRARGLSRPROAAVCAVLMVLVIGSLVARWLLGIQEGGFCFRSTRHFNFSMRPPLIGF 180  
QY 181 YLPLAVVVFCSLKVVTAQAQPPTDVGOAEATRKAKRMVWNLVVFVCFPLPHVGLTVR 240  
Db 181 YLPLAVVVFCSLKVVTAQAQPPTDVGOAEATRKAKRMVWNLVVFVCFPLPHVGLTVR 240  
QY 241 LAVGNACALLETIRRALYITSLKSDANCCCLDAICYYMAKEFQBSALAVAPRAKAHKS 300  
Db 241 LAVGNACALLETIRRALYITSLKSDANCCCLDAICYYMAKEFQBSALAVAPRAKAHKS 300  
QY 301 QDSLVCVTLA 309  
Db 301 QDSLVCVTLA 309

## RESULT 4

US-10-505-486-84  
; Sequence 84, Application US/10505486  
; Publication No. US20050118639A1  
; GENERAL INFORMATION:  
; APPLICANT: Takeda Chemical Industries, Ltd.  
; TITLE OF INVENTION: Determination of a ligand  
; FILE REFERENCE: P03-0006PCT  
; CURRENT APPLICATION NUMBER: US/10/505,486  
; CURRENT FILING DATE: 2004-08-20  
; PRIOR APPLICATION NUMBER: JP 2002-45728  
; PRIOR FILING DATE: 2002-02-22  
; PRIOR APPLICATION NUMBER: JP 2002-213949  
; PRIOR FILING DATE: 2002-07-23  
; PRIOR APPLICATION NUMBER: JP 2002-298237  
; PRIOR FILING DATE: 2002-10-11  
; NUMBER OF SEQ ID NOS: 233  
; SEQ ID NO 84  
; LENGTH: 547  
; TYPE: PRT  
; ORGANISM: Human  
US-10-505-486-84

Query Match 99.3%; Score 1603; DB 5; Length 547;  
Best Local Similarity 99.4%; Pred. No. 5.1e-146;  
Matches 307; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MNGTYNTCGSSDLTPWPPAIKLGFYAYLGVLVLLGLLNSLALWVFCRMOQWTETRIYMT 60  
Db 1 MNGTYNTCGSSDLTPWPPAIKLGFYAYLGVLVLLGLLNSLALWVFCRMOQWTETRIYMT 60  
QY 61 NLAVADCLLCTLPFVLSLRDTSPTPLCQLSQGIYLTNRYSISLVTIAVDRYVAVRH 120  
Db 61 NLAVADCLLCTLPFVLSLRDTSPTPLCQLSQGIYLTNRYSISLVTIAVDRYVAVRH 120  
QY 121 PLRARGLSRPROAAVCAVLMVLVIGSLVARWLLGIQEGGFCFRSTRHFNFSMRPPLIGF 180

Db 121 PLRAGRLSPQAAAVCAVLWLVIGSLVARWLLGIGEGGCFRSTRNFNSMAFPLG 180  
Qy 181 YLPLAVVFCSLKVVTTALAQRPPTDVGOAETRAKAKMWMANLLVFFVCFPLHVLTVR 240  
Db 181 YLPLAVVFCSLKVVTTALAQRPPTDVGOAETRAKAKMWMANLLVFFVCFPLHVLTVR 240  
Qy 241 LAVGNACALLETIRRALYITSKLSDANCCLDACIYYWAKEFOEASALAVAPRAKAHS 300  
Db 241 LAVGNACALLETIRRALYITSKLSDANCCLDACIYYWAKEFOEASALAVAPRAKAHS 300  
Qy 301 QDSLCTVTLA 309  
Db 301 QDSLCTVTLA 309

RESULT 5  
US-10-157-031-351  
; Sequence 351, Application US/10157031  
; Publication No. US20030108890A1  
; GENERAL INFORMATION:  
; APPLICANT: Baranova, A. V.  
; APPLICANT: Yankovsky, N. K.  
; APPLICANT: Kozlov, A. P.  
; APPLICANT: Lobashev, A. V.  
; APPLICANT: Krukovskaya, L. L.  
; TITLE OF INVENTION: In silico screening for phenotype-associated expressed sequences  
; FILE REFERENCE: 2760-103  
; CURRENT APPLICATION NUMBER: US/10/157,031  
; CURRENT FILING DATE: 2002-05-30  
; NUMBER OF SEQ ID NOS: 415  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 351  
; LENGTH: 309  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-157-031-351

Query Match 98.9%; Score 1597; DB 4; Length 309;  
Best Local Similarity 99.0%; Pred. No. 9.9e-146;  
Matches 306; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Qy 1 MNGTYNTCGSDLTWPPAKLGFYAYLGVLLVIGLLNSLALWVPCCRMQOWTETRIYMT 60  
Db 1 MNGTYNTCGSDLTWPPAKLGFYAYLGVLLVIGLLNSLALWVPCCRMQOWTETRIYMT 60  
Qy 61 NLAVADICLLCTLPFVLSLRDTSPLCQLSQGIYLTNRYSISLVTAIAVDRYAVRH 120  
Db 61 NLAVADICLLCTLPFVLSLRDTSPLCQLSQGIYLTNRYSISLVTAIAVDRYAVRH 120  
Qy 121 PLRAGRLSPQAAAVCAVLWLVIGSLVARWLLGIGEGGCFRSTRNFNSMRPPLIGF 180  
Db 121 PLRAGRLSPQAAAVCAVLWLVIGSLVARWLLGIGEGGCFRSTRNFNSMAFPLG 180  
Qy 181 YLPLAVVFCSLKVVTTALAQRPPTDVGOAETRAKAKMWMANLLVFFVCFPLHVLTVR 240  
Db 181 YLPLAVVFCSLKVVTTALAQRPPTDVGOAETRAKAKMWMANLLVFFVCFPLHVLTVR 240  
Qy 241 LAVGNACALLETIRRALYITSKLSDANCCLDACIYYWAKEFOEASALAVAPRAKAHS 300  
Db 241 LAVGNACALLETIRRALYITSKLSDANCCLDACIYYWAKEFOEASALAVAPRAKAHS 300  
Qy 301 QDSLCTVTLA 309  
Db 301 QDSLCTVTLA 309

RESULT 6  
US-09-964-821B-11  
; Sequence 11, Application US/09964821B  
; Publication No. US20030186360A1  
; GENERAL INFORMATION:  
; APPLICANT: FEDER, J. N.

; APPLICANT: MINTIER, G.  
; APPLICANT: RAMANATHAN, C. S.  
; APPLICANT: HAWKEN, D.R.  
; APPLICANT: CACACE, A.  
; APPLICANT: BARBER, L.  
; APPLICANT: KORNACKER, M. G.  
; TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPBMY3,  
; FILE REFERENCE: D0042NP  
; CURRENT APPLICATION NUMBER: US/09/964,821B  
; CURRENT FILING DATE: 2002-06-10  
; PRIOR APPLICATION NUMBER: 60/235,713  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: 60/261,783  
; PRIOR FILING DATE: 2001-01-17  
; PRIOR APPLICATION NUMBER: 60/305,085  
; PRIOR FILING DATE: 2001-07-13  
; PRIOR APPLICATION NUMBER: 60/313,171  
; PRIOR FILING DATE: 2001-08-17  
; NUMBER OF SEQ ID NOS: 63  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 11  
; LENGTH: 370  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-964-821B-11

Query Match 24.8%; Score 401; DB 3; Length 370;  
Best Local Similarity 34.1%; Pred. No. 4.1e-30;  
Matches 103; Conservative 60; Mismatches 11; Indels 28; Gaps 10;  
Qy 25 AYLGVLVLLGLLNSLALWVPCCRMQOWTETRIYMTNLAVADICLLCTLPF-VLHSLR-- 81  
Db 44 AVYSVVFILGILITNSVLSLFPVCFEMKMRSEITAITNLAVSDLLFVCTLPFKIPFNHRH 103  
Qy 82 -DTSPTPLCQLSQGIYLTNRYSISLVTAIAVDRYAVRHPLRAGRLSPQAAAVCAVL 140  
Db 104 WPPGDT-LCKISGTAFLTNIYGSMLFLTICISVDRFLAIVPFRSRTIRTRNSAIVCAGV 162  
Qy 141 WLVIGSLVARWLLGIGQ-----GGCFRSTRNFNSMR--FPLLGFLVPLAVVVF 189  
Db 163 WILVLSGGISASLSTNNVNNATTCPEGFSKRWKTKITIFIEVVGFIIPILNVS 222  
Qy 190 CSLKVVTTALAQRPPTDVGOAET-RKAKRMWMANLLVFFVCFPLHVLTVRLAVGNAC 248  
Db 223 CSSVVLRTL--RKATLSQIGTKNKKVLMITVMAVFFVCFVPSVLFYALVRSQAI 280  
Qy 249 --ALLETIRRALY-ITSKLSANCCLDACIYYWAKEFOEASALAVAPRAKAHSQDSLC 305  
Db 281 TNCFLERPAKIMYPITLCLATLNCFCDFPIYFTLESQKGFYI-----NAHIRMESLIF 334  
Qy 306 VT 307  
Db 335 KT 336

RESULT 7  
US-10-081-810-44  
; Sequence 44, Application US/10081810  
; Publication No. US20030064438A1  
; GENERAL INFORMATION:  
; APPLICANT: Bristol-Myers Squibb Company  
; TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTOR NUCLEIC ACIDS, POLYPEPTIDES, ANTIBODI-  
; FILE REFERENCE: D0132 NP  
; CURRENT APPLICATION NUMBER: US/10/081,810  
; CURRENT FILING DATE: 2002-02-22  
; PRIOR APPLICATION NUMBER: US 60/270,793  
; PRIOR FILING DATE: 2001-02-23  
; PRIOR APPLICATION NUMBER: US 60/270,792  
; PRIOR FILING DATE: 2001-02-23  
; PRIOR APPLICATION NUMBER: US 60/296,427  
; PRIOR FILING DATE: 2001-06-06

```
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 44
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-081-810-44

Query Match      24.8%; Score 401; DB 4; Length 370;
Best Local Similarity 34.1%; Pred. No. 4.1e-30;
Matches 103; Conservative 60; Mismatches 111; Indels 28; Gaps 10;

QY 25 AVLGVLVGLLLNSLALWVFCRMOQWETRIYMTNLAVADICLLCTLPF-VLHSLR-- 81
Db 44 AVYSVVFILGLITNSVLSVFCFRMKMRSETAIFITNLAVSDLLFVCTLPFKIFYNFRH 103

QY 82 -DTSDFPLCOLSGIYLTNRYSISLVTAIVDRYVAVRHPLRARGLRSPROAAACAVL 140
Db 104 WPGDGT-LCKISGTAFLTNIYGSMLFLTCISVDRFLAIYVPPRSRTIRTRNSAIVCAGV 162

QY 141 WLVIGSLVARMLLGIOE-----GGFCFRSTRHNFSMR--PPLIGFYPLAVVVVF 189
Db 163 WILVSGGISASLFSFTNNVNNATTCFEGFSKRVKTYLSKITPIETVGVGFIPLINVS 222

QY 190 CSLKVVTALAQRPTDVGQAEAT-RKAKRMVWANLLVVFVCPFLPHVGLTVRLAVGWNAC 248
Db 223 CSSVVLRTL--RKPATLSQIGTNKKKVLKMITVHMAVVFVCFVYNSVLFVALVRSQAI 280

QY 249 --ALLETIRRALY-ITSKLSDANCCCLDAICYYYMAKEFOEASALAVAPRAKAHKSODSLC 305
Db 281 TNCFLERPAKIMYPITLCLATLNCCDFPIYFTLESFQKSFYI-----NAHIRMESLF 334

QY 306 VT 307
Db 335 KT 336

RESULT 8
US-10-225-567A-225
; Sequence 225, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; PRIOR FILING DATE: 2001-12-19
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 225
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-225

Query Match      24.8%; Score 401; DB 4; Length 370;
Best Local Similarity 34.1%; Pred. No. 4.1e-30;
Matches 103; Conservative 60; Mismatches 111; Indels 28; Gaps 10;

QY 25 AVLGVLVGLLLNSLALWVFCRMOQWETRIYMTNLAVADICLLCTLPF-VLHSLR-- 81
Db 44 AVYSVVFILGLITNSVLSVFCFRMKMRSETAIFITNLAVSDLLFVCTLPFKIFYNFRH 103

QY 82 -DTSDFPLCOLSGIYLTNRYSISLVTAIVDRYVAVRHPLRARGLRSPROAAACAVL 140
Db 104 WPGDGT-LCKISGTAFLTNIYGSMLFLTCISVDRFLAIYVPPRSRTIRTRNSAIVCAGV 162

QY 141 WLVIGSLVARMLLGIOE-----GGFCFRSTRHNFSMR--PPLIGFYPLAVVVVF 189
Db 281 TNCFLERPAKIMYPITLCLATLNCCDFPIYFTLESFQKSFYI-----NAHIRMESLF 334
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; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 44
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-081-810-44

Query Match      24.8%; Score 401; DB 4; Length 370;
Best Local Similarity 34.1%; Pred. No. 4.1e-30;
Matches 103; Conservative 60; Mismatches 111; Indels 28; Gaps 10;

QY 25 AVLGVLVGLLLNSLALWVFCRMOQWETRIYMTNLAVADICLLCTLPF-VLHSLR-- 81
Db 44 AVYSVVFILGLITNSVLSVFCFRMKMRSETAIFITNLAVSDLLFVCTLPFKIFYNFRH 103

QY 82 -DTSDFPLCOLSGIYLTNRYSISLVTAIVDRYVAVRHPLRARGLRSPROAAACAVL 140
Db 104 WPGDGT-LCKISGTAFLTNIYGSMLFLTCISVDRFLAIYVPPRSRTIRTRNSAIVCAGV 162

QY 141 WLVIGSLVARMLLGIOE-----GGFCFRSTRHNFSMR--PPLIGFYPLAVVVVF 189
Db 163 WILVSGGISASLFSFTNNVNNATTCFEGFSKRVKTYLSKITPIETVGVGFIPLINVS 222

QY 190 CSLKVVTALAQRPTDVGQAEAT-RKAKRMVWANLLVVFVCPFLPHVGLTVRLAVGWNAC 248
Db 223 CSSVVLRTL--RKPATLSQIGTNKKKVLKMITVHMAVVFVCFVYNSVLFVALVRSQAI 280

QY 249 --ALLETIRRALY-ITSKLSDANCCCLDAICYYYMAKEFOEASALAVAPRAKAHKSODSLC 305
Db 281 TNCFLERPAKIMYPITLCLATLNCCDFPIYFTLESFQKSFYI-----NAHIRMESLF 334

QY 306 VT 307
Db 335 KT 336

RESULT 9
US-10-024-298A-176
; Sequence 176, Application US/10024298A
; Publication No. US20030143540A1
; GENERAL INFORMATION:
; APPLICANT: ASAHI KASEI KABUSHIKI KAISHA
; APPLICANT: AKIO MATSUDA
; APPLICANT: Goichi HONDA
; APPLICANT: Shuji MURAMATSU
; APPLICANT: Yukiko NAGANO
; TITLE OF INVENTION: NF-K B Activating Gene
; FILE REFERENCE: 1254-0191P
; CURRENT APPLICATION NUMBER: US/10/024,298A
; CURRENT FILING DATE: 2003-04-08
; PRIOR APPLICATION NUMBER: 60/314,385
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 60/278,641
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: 60/258,315
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: JP254018/2001
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: JP008912/2001
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: JP402288/2000
; PRIOR FILING DATE: 2000-12-28
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 176
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-024-298A-176

Query Match      24.8%; Score 401; DB 4; Length 370;
Best Local Similarity 34.1%; Pred. No. 4.1e-30;
Matches 103; Conservative 60; Mismatches 111; Indels 28; Gaps 10;

QY 25 AVLGVLVGLLLNSLALWVFCRMOQWETRIYMTNLAVADICLLCTLPF-VLHSLR-- 81
Db 44 AVYSVVFILGLITNSVLSVFCFRMKMRSETAIFITNLAVSDLLFVCTLPFKIFYNFRH 103

QY 82 -DTSDFPLCOLSGIYLTNRYSISLVTAIVDRYVAVRHPLRARGLRSPROAAACAVL 140
Db 104 WPGDGT-LCKISGTAFLTNIYGSMLFLTCISVDRFLAIYVPPRSRTIRTRNSAIVCAGV 162

QY 141 WLVIGSLVARMLLGIOE-----GGFCFRSTRHNFSMR--PPLIGFYPLAVVVVF 189
Db 163 WILVSGGISASLFSFTNNVNNATTCFEGFSKRVKTYLSKITPIETVGVGFIPLINVS 222

QY 190 CSLKVVTALAQRPTDVGQAEAT-RKAKRMVWANLLVVFVCPFLPHVGLTVRLAVGWNAC 248
Db 223 CSSVVLRTL--RKPATLSQIGTNKKKVLKMITVHMAVVFVCFVYNSVLFVALVRSQAI 280

QY 249 --ALLETIRRALY-ITSKLSDANCCCLDAICYYYMAKEFOEASALAVAPRAKAHKSODSLC 305
Db 281 TNCFLERPAKIMYPITLCLATLNCCDFPIYFTLESFQKSFYI-----NAHIRMESLF 334
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QY 306 VT 307  
DB 335 KT 336

RESULT 10

US-10-042-211A-176  
; Sequence 176, Application US/10042211A  
; Publication No. US20030170719A1  
; GENERAL INFORMATION:  
; APPLICANT: MATSUDA, Akio et al.  
; TITLE OF INVENTION: NFkB Activating Gene  
; FILE REFERENCE: 1254-0192P  
; CURRENT APPLICATION NUMBER: US/10/042,211A  
; CURRENT FILING DATE: 2002-01-11  
; PRIOR APPLICATION NUMBER: JP 2000-402288  
; PRIOR FILING DATE: 2000-12-28  
; PRIOR APPLICATION NUMBER: JP 2001-088912  
; PRIOR FILING DATE: 2001-03-26  
; PRIOR APPLICATION NUMBER: JP 2001-254018  
; PRIOR FILING DATE: 2001-08-24  
; PRIOR APPLICATION NUMBER: US 60/258,315  
; PRIOR FILING DATE: 2000-12-28  
; PRIOR APPLICATION NUMBER: US 60/278,640  
; PRIOR FILING DATE: 2001-03-26  
; PRIOR APPLICATION NUMBER: US 60/314,385  
; PRIOR FILING DATE: 2001-08-24  
; NUMBER OF SEQ ID NOS: 182  
; SOFTWARE: Patent In Ver. 2.0  
; SEQ ID NO 176  
; LENGTH: 370  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-042-211A-176

Query Match 24.8%; Score 401; DB 4; Length 370;

Best Local Similarity 34.1%; Pred. No. 4.1e-30;  
Matches 103; Conservative 60; Mismatches 111; Indels 28; Gaps 10;

QY 25 AYLGVLVLLGLLNSLALVFCRCMQWTTETRIYMTNLAVADLCLLCTLPF-VLHSLR-- 81  
DB 44 AVYSVVFILGLITNSVSLFVFCFRMKRSETAIFITNLAVSDLLFVCTLPFKIFYNFRH 103  
QY 82 -DTSPTLCQLSQGIYLTNRYSISLVTAIVDRVAVRHPLRARGLSRQQAACAVL 140  
DB 104 WPFQGT-LCKISGTAFTLNIYGSMLFCLTICISVDRELAIVPFRSRTIIRNSAIVCAGV 162  
QY 141 WVLVIGSLVARWLLGIQ-----GGFCFRSTRHNFSMR--FPLLGFYLPVAVVF 189  
DB 163 WILVLSGGISASLSTTNVNNATTTCFEGFSKRVKTKYLSKITIFIEVVGFIIPILNVS 222  
QY 190 CSLKVVVTAQAORPPTDVQAEAT-RKAKRMVWNLVFFVVCFLPLHLVGLTVRLAVGWNAC 248  
DB 223 CSSVVLRTL--RKPAITLSQIGTNKKVKLKMIVHMAVFFVCFVPSVLFYALVRSQAI 280  
QY 249 --ALLETIRRALY-ITSKLSANCLDAICYYIMAKFQESALAVAPRAKAKHSQDSLC 305  
DB 281 TNCFLERPAKIMYPITLCLATLNCDFDPFIYFTLESFQKSFYI-----NAHIRMESLF 334  
QY 306 VT 307  
DB 335 KT 336

RESULT 11

US-10-268-332-11  
; Sequence 11, Application US/10268332  
; Publication No. US20030175748A1  
; GENERAL INFORMATION:  
; APPLICANT: Bristol-Myers Squibb Company  
; TITLE OF INVENTION: NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPRBMV3, EXPRESSED HIGHLY  
; TITLE OF INVENTION: IMMUNE- AND COLON- RELATED TISSUES

FILE REFERENCE: D0042A CIP  
; CURRENT APPLICATION NUMBER: US/10/268,332  
; CURRENT FILING DATE: 2002-10-10  
; PRIOR APPLICATION NUMBER: U.S. 60/235,713  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: U.S. 60/261,783  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: U.S. 60/305,085  
; PRIOR FILING DATE: 2001-07-13  
; PRIOR APPLICATION NUMBER: U.S. 60/313,171  
; PRIOR FILING DATE: 2001-08-17  
; PRIOR APPLICATION NUMBER: U.S. 09/964,821  
; PRIOR FILING DATE: 2001-09-26  
; NUMBER OF SEQ ID NOS: 66  
; SOFTWARE: Patent In version 3.1  
; SEQ ID NO 11  
; LENGTH: 370  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-268-332-11

Query Match 24.8%; Score 401; DB 4; Length 370;

Best Local Similarity 34.1%; Pred. No. 4.1e-30;  
Matches 103; Conservative 60; Mismatches 111; Indels 28; Gaps 10;

QY 25 AYLGVLVLLGLLNSLALVFCRCMQWTTETRIYMTNLAVADLCLLCTLPF-VLHSLR-- 81  
DB 44 AVYSVVFILGLITNSVSLFVFCFRMKRSETAIFITNLAVSDLLFVCTLPFKIFYNFRH 103  
QY 82 -DTSPTLCQLSQGIYLTNRYSISLVTAIVDRVAVRHPLRARGLSRQQAACAVL 140  
DB 104 WPFQGT-LCKISGTAFTLNIYGSMLFCLTICISVDRELAIVPFRSRTIIRNSAIVCAGV 162  
QY 141 WVLVIGSLVARWLLGIQ-----GGFCFRSTRHNFSMR--FPLLGFYLPVAVVF 189  
DB 163 WILVLSGGISASLSTTNVNNATTTCFEGFSKRVKTKYLSKITIFIEVVGFIIPILNVS 222  
QY 190 CSLKVVVTAQAORPPTDVQAEAT-RKAKRMVWNLVFFVVCFLPLHLVGLTVRLAVGWNAC 248  
DB 223 CSSVVLRTL--RKPAITLSQIGTNKKVKLKMIVHMAVFFVCFVPSVLFYALVRSQAI 280  
QY 249 --ALLETIRRALY-ITSKLSANCLDAICYYIMAKFQESALAVAPRAKAKHSQDSLC 305  
DB 281 TNCFLERPAKIMYPITLCLATLNCDFDPFIYFTLESFQKSFYI-----NAHIRMESLF 334  
QY 306 VT 307  
DB 335 KT 336

RESULT 12

US-10-617-217A-176  
; Sequence 176, Application US/10617217A  
; Publication No. US20040081986A1  
; GENERAL INFORMATION:  
; APPLICANT: MATSUDA, Akio et al.  
; TITLE OF INVENTION: NF-kB ACTIVATING GENE  
; FILE REFERENCE: 1254-0229P  
; CURRENT APPLICATION NUMBER: US/10/617,217A  
; CURRENT FILING DATE: 2003-07-11  
; PRIOR APPLICATION NUMBER: JP 2000-402288  
; PRIOR FILING DATE: 2000-12-28  
; PRIOR APPLICATION NUMBER: JP 2001-088912  
; PRIOR FILING DATE: 2001-03-26  
; PRIOR APPLICATION NUMBER: JP 2001-254018  
; PRIOR FILING DATE: 2001-08-24  
; PRIOR APPLICATION NUMBER: US 60/258,315  
; PRIOR FILING DATE: 2000-12-28  
; PRIOR APPLICATION NUMBER: US 60/278,640  
; PRIOR FILING DATE: 2001-03-26  
; PRIOR APPLICATION NUMBER: US 60/314,385  
; PRIOR FILING DATE: 2001-08-24  
; NUMBER OF SEQ ID NOS: 224

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/ SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 176
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-617-217A-176

Query Match          24.8%; Score 401; DB 4; Length 370;
Best Local Similarity 34.1%; Pred. No. 4.1e-30;
Matches 103; Conservative 60; Mismatches 111; Indels 28; Gaps 10;

QY 25 AYLGVLVLLGLLNSLALWVFCRCMQWETRIYMTNLAVADLCCLCTLPF-VLHSLR-- 81
DB 44 AVYSVVFIGLITNSVLSLVFCFRMKRSETAIFITNLAVSDLLFVCTLPFKIFYNFRH 103
QY 82 -DTSDFPLCOLSGIYLTNRNMSISLVTAIVDRYVAVRHPLRARGLSRQQAACAVL 140
DB 104 WPFQDT-LCKISGTAFITNIYGMFLFTCISVDRFLAIVYPPFRSRTIRTRNSAIVCAGV 162
QY 141 WLVIGSLVARWMLGTOE-----GGFCFRSTRHNFNSMR--PPLLGFYLPPLAVVVF 189
DB 163 WILVSGGISASLFSFTTNVNNATTCFEGFSKRWKTYLSKITIFIEVVGFIIPLINVS 222
QY 190 CSLKVVVTTALAQRPPTDVGOAEAT-RKAKRMVWVWVNLVFFVCPFLPHVGLTVRLAVGWNAC 248
DB 223 CSSVVLRTL--RKPATLSQIGTNKKVLMKMTVHMAVFFVCFVYNSVLFYALVRSQAI 280
QY 249 --ALLETIRRALY-ITSKLSANDCCCLDAICYTMAKEFOEASALAVAPRAKAHKSQDSL 305
DB 281 TNCFLERPAKIMYPITCLATLNCPCDPPIYYFTLESFQKSFYI-----NAHIRMESLP 334
QY 306 VT 307
DB 335 KT 336

RESULT 14
US-10-024-298A-176
; Sequence 176, Application US/10024298A
; Publication No. US20040214167A9
; GENERAL INFORMATION:
; APPLICANT: ASAH KASEI KABUSHIKI KAISHA
; APPLICANT: AKIO MATSUDA
; APPLICANT: Goichi HONDA
; APPLICANT: Shuji MURAMATSU
; APPLICANT: Yukiko NAGANO
; TITLE OF INVENTION: NF-K B Activating Gene
; FILE REFERENCE: 1254-0191P
; CURRENT APPLICATION NUMBER: US/10/024,298A
; CURRENT FILING DATE: 2003-04-08
; PRIOR APPLICATION NUMBER: 60/314,385
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 60/278,641
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: 60/258,315
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: JP254018/2001
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: JP0088912/2001
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: JP402288/2000
; PRIOR FILING DATE: 2000-12-28
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 176
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-024-298A-176

Query Match          24.8%; Score 401; DB 4; Length 370;
Best Local Similarity 34.1%; Pred. No. 4.1e-30;
Matches 103; Conservative 60; Mismatches 111; Indels 28; Gaps 10;

QY 25 AYLGVLVLLGLLNSLALWVFCRCMQWETRIYMTNLAVADLCCLCTLPF-VLHSLR-- 81
DB 44 AVYSVVFIGLITNSVLSLVFCFRMKRSETAIFITNLAVSDLLFVCTLPFKIFYNFRH 103
QY 82 -DTSDFPLCOLSGIYLTNRNMSISLVTAIVDRYVAVRHPLRARGLSRQQAACAVL 140
DB 104 WPFQDT-LCKISGTAFITNIYGMFLFTCISVDRFLAIVYPPFRSRTIRTRNSAIVCAGV 162
QY 141 WLVIGSLVARWMLGTOE-----GGFCFRSTRHNFNSMR--PPLLGFYLPPLAVVVF 189
DB 163 WILVSGGISASLFSFTTNVNNATTCFEGFSKRWKTYLSKITIFIEVVGFIIPLINVS 222
QY 190 CSLKVVVTTALAQRPPTDVGOAEAT-RKAKRMVWVWNLVFFVCPFLPHVGLTVRLAVGWNAC 248
DB 223 CSSVVLRTL--RKPATLSQIGTNKKVLMKMTVHMAVFFVCFVYNSVLFYALVRSQAI 280
QY 249 --ALLETIRRALY-ITSKLSANDCCCLDAICYTMAKEFOEASALAVAPRAKAHKSQDSL 305
DB 281 TNCFLERPAKIMYPITCLATLNCPCDPPIYYFTLESFQKSFYI-----NAHIRMESLP 334
QY 306 VT 307
DB 335 KT 336

RESULT 13
US-10-775-965-11
; Sequence 11, Application US/10775965
; Publication No. US20040209808A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; APPLICANT: Kornacker, Michael
; TITLE OF INVENTION: MODULATORS OF HUMAN G-PROTEIN COUPLED RECEPTORS
; FILE REFERENCE: D0286 NP
; CURRENT APPLICATION NUMBER: US/10/775,965
; CURRENT FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: U.S. 60/446,655
; PRIOR FILING DATE: 2003-02-11
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 11
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-775-965-11

Query Match          24.8%; Score 401; DB 4; Length 370;
Best Local Similarity 34.1%; Pred. No. 4.1e-30;
Matches 103; Conservative 60; Mismatches 111; Indels 28; Gaps 10;

QY 25 AYLGVLVLLGLLNSLALWVFCRCMQWETRIYMTNLAVADLCCLCTLPF-VLHSLR-- 81
DB 44 AVYSVVFIGLITNSVLSLVFCFRMKRSETAIFITNLAVSDLLFVCTLPFKIFYNFRH 103
QY 82 -DTSDFPLCOLSGIYLTNRNMSISLVTAIVDRYVAVRHPLRARGLSRQQAACAVL 140
DB 104 WPFQDT-LCKISGTAFITNIYGMFLFTCISVDRFLAIVYPPFRSRTIRTRNSAIVCAGV 162
QY 141 WLVIGSLVARWMLGTOE-----GGFCFRSTRHNFNSMR--PPLLGFYLPPLAVVVF 189
DB 163 WILVSGGISASLFSFTTNVNNATTCFEGFSKRWKTYLSKITIFIEVVGFIIPLINVS 222
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Db 335 KT 336

RESULT 15

US-10-753-267-86

Sequence 86, Application US/10753267

Publication No. US20050037946A1

GENERAL INFORMATION:

APPLICANT: Millennium Pharmaceuticals, Inc.

APPLICANT: Stegaliano, Nancy E.

APPLICANT: Healy, Aileen

APPLICANT: Acton, Susan L.

APPLICANT: Galvin, Katherine M.

APPLICANT: Donoghue, Mary A.

APPLICANT: Rodriguez-Way, Amelie

APPLICANT: Tomlinson, James E.

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING

TITLE OF INVENTION: CARDIOVASCULAR DISEASE USING 1722, 10280, 59917, 85553,

TITLE OF INVENTION: 10653, 9235, 21668, 17794, 2210, 6169, 10102, 21061, 17662,

TITLE OF INVENTION: 1468, 12282, 6350, 9035, 1820, 23652, 7301, 8925, 8701,

TITLE OF INVENTION: 3533, 9462, 9123, 12788, 17729, 65552, 1261, 21476, 33770,

TITLE OF INVENTION: 9380, 2569654, 33556, 44143, 32612, 10671, 261.

TITLE OF INVENTION: 44570, 41922, 2552, 2417, 19319, 43969, 8921, 8993, 955,

TITLE OF INVENTION: 32345, 966, 1920, 17318, 1510, 14180, 26005, 554, 16408,

TITLE OF INVENTION: 42028, 112091, 13886, 13942, 1673, 54946 OR 2419

FILE REFERENCE: MPI03-003P1RNMNIM

CURRENT APPLICATION NUMBER: US/10/753,267

CURRENT FILING DATE: 2004-01-08

PRIOR APPLICATION NUMBER: US 60/439,683

PRIOR FILING DATE: 2003-01-13

PRIOR APPLICATION NUMBER: US 60/445,216

PRIOR FILING DATE: 2003-02-05

PRIOR APPLICATION NUMBER: US 60/448,036

PRIOR FILING DATE: 2003-02-18

PRIOR APPLICATION NUMBER: US 60/454,189

PRIOR FILING DATE: 2003-03-12

PRIOR APPLICATION NUMBER: US 60/457,541

PRIOR FILING DATE: 2003-03-25

PRIOR APPLICATION NUMBER: US 60/466,411

PRIOR FILING DATE: 2003-04-29

PRIOR APPLICATION NUMBER: US 60/469,041

PRIOR FILING DATE: 2003-05-08

PRIOR APPLICATION NUMBER: US 60/477,414

PRIOR FILING DATE: 2003-06-10

PRIOR APPLICATION NUMBER: US 60/478,560

PRIOR FILING DATE: 2003-06-13

PRIOR APPLICATION NUMBER: US 60/489,772

PRIOR FILING DATE: 2003-07-24

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 130

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 86

LENGTH: 370

TYPE: PRT

ORGANISM: Homo Sapiens

US-10-753-267-86

Search completed: February 9, 2006, 01:21:15

Job time : 118.5 secs

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Db 223 CSSVWLRTL--RKPATLSQIGTNNKKVLMITVHMAVVFVVCFLPLHVLTVRLAVGNAC 280

QY 249 --ALLETTIRALY-ITSKLSDANCCCLDAICVYYWAKEFOEASALAVAPRAKAKHSQDSLC 305

Db 281 TNCFLERFAKIMYPITLCLATLNCCTDPFIYITLESFQKSYI-----NAHIRMESLP 334

QY 306 VT 307

Db 335 KT 336

Query Match 24.8%; Score 401; DB 5; Length 370;

Best Local Similarity 34.1%; Pred. No. 4.1e-30;

Matches 103; Conservative 60; Mismatches 111; Indels 28; Gaps 10;

QY 25 AYGLVLLVGLLLNLALWFCRQQWQWTTETIYMTNLAVADICLLCTLPF-VLHSLR-- 81

Db 44 AVYSVVFILGLITNSVSLVFCFRMKMRSETAIFITNLAVSDLLFVCTLPFKIFYNFRH 103

QY 82 -DTSFTPLCOLSQGIYLTNRVMSISLVTAIVDVAVVHPLRARGLSRPROAAACAVL 140

Db 104 WPFQGT-LCKISGTAPLTNIYSGMLFLTCISVDRFLAIVYPRRTIRNRSAIVCAGV 162

QY 141 WVLVTGLSVARWLGLQIE-----GGFCFRSTRHNFSNMR--PPLIGFYLP LAVVVF 189

Db 163 WILVLSGGISASLFTSTNNATTTTCFEGFSKRVKWTLSKITIFIEVVGFIIPLILNV 222

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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 9, 2006, 01:17:29 ; Search time 10.5 Seconds  
(without alignments)  
386.178 Million cell updates/sec

Title: US-10-083-168-85

Perfect score: 1615

Sequence: 1 MNGTYTCGSSDLTWPAIK.....AVAPRAKHSQDSLCVTILA 309

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 97014 seqs, 13122538 residues

Total number of hits satisfying chosen parameters: 97014

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New:\*

- 1: /cgn2\_6/ptodata/1/pubaa/US08 NEW PUB.pap.\*
- 2: /cgn2\_6/ptodata/1/pubaa/US06 NEW PUB.pap.\*
- 3: /cgn2\_6/ptodata/1/pubaa/US07 NEW PUB.pap.\*
- 4: /cgn2\_6/ptodata/1/pubaa/PCT NEW PUB.pap.\*
- 5: /cgn2\_6/ptodata/1/pubaa/US09 NEW PUB.pap.\*
- 6: /cgn2\_6/ptodata/1/pubaa/US10 NEW PUB.pap.\*
- 7: /cgn2\_6/ptodata/1/pubaa/US11 NEW PUB.pap.\*
- 8: /cgn2\_6/ptodata/1/pubaa/US60 NEW PUB.pap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description          |
|------------|-------|-------------|--------|----|----------------------|
| 1          | 329.5 | 20.4        | 254    | 6  | US-10-055-877-248    |
| 2          | 329.5 | 20.4        | 254    | 6  | US-10-055-877-327    |
| 3          | 329.5 | 20.4        | 254    | 6  | US-10-055-877-340    |
| 4          | 329.5 | 20.4        | 254    | 6  | US-10-055-877-346-83 |
| 5          | 316.5 | 19.6        | 346    | 7  | US-11-157-930-2      |
| 6          | 315.5 | 19.5        | 365    | 6  | US-10-055-877-545    |
| 7          | 311.5 | 19.3        | 391    | 7  | US-11-127-877-52     |
| 8          | 300   | 18.6        | 259    | 6  | US-10-055-877-225    |
| 9          | 300   | 18.6        | 259    | 6  | US-10-055-877-237    |
| 10         | 298   | 18.5        | 339    | 7  | US-11-157-930-4      |
| 11         | 298   | 18.5        | 367    | 7  | US-11-157-930-6      |
| 12         | 297.5 | 18.4        | 358    | 7  | US-11-127-877-66     |
| 13         | 296.5 | 18.4        | 373    | 7  | US-11-127-877-46     |
| 14         | 286.5 | 17.7        | 352    | 6  | US-10-055-877-523    |
| 15         | 286.5 | 17.7        | 352    | 7  | US-11-068-686-2      |
| 16         | 286.5 | 17.7        | 352    | 7  | US-11-127-877-61     |
| 17         | 285.5 | 17.7        | 352    | 7  | US-11-068-686-20     |
| 18         | 273.5 | 16.9        | 337    | 7  | US-11-157-930-5      |
| 19         | 273.5 | 16.9        | 375    | 7  | US-11-127-877-67     |
| 20         | 261.5 | 16.2        | 374    | 7  | US-11-127-877-62     |
| 21         | 255.5 | 15.8        | 359    | 6  | US-10-055-877-712    |
| 22         | 255.5 | 15.8        | 359    | 6  | US-10-055-877-716    |
| 23         | 255.5 | 15.8        | 359    | 6  | US-10-055-877-716    |
| 24         | 255.5 | 15.8        | 359    | 7  | US-11-127-877-65     |
| 25         | 255.5 | 15.8        | 388    | 6  | US-10-055-877-713    |

Sequence 714, App  
Sequence 715, App  
Sequence 55, Appl  
Sequence 934, App  
Sequence 838, App  
Sequence 837, App  
Sequence 2, Appli  
Sequence 60, Appl  
Sequence 161, App  
Sequence 4, Appli  
Sequence 4, Appli  
Sequence 36, Appl  
Sequence 12, Appl  
Sequence 24, Appl  
Sequence 636, App  
Sequence 637, App  
Sequence 6, Appli  
Sequence 59, Appl  
Sequence 32, Appl

#### ALIGNMENTS

#### RESULT 1

US-10-055-877-248  
; Sequence 248, Application US/10055877  
; Publication No. US20050289241A1

#### GENERAL INFORMATION:

; APPLICANT: Decristofaro, Marc  
; APPLICANT: Padigar, Murallidhara  
; APPLICANT: Miller, Charles  
; APPLICANT: Tchernev, Velizar  
; APPLICANT: Zhong, Mei  
; APPLICANT: Anderson, David  
; APPLICANT: Ballinger, Robert  
; APPLICANT: Gerlach, Valerie  
; APPLICANT: Spytek, Kimberly  
; APPLICANT: Ratelli, Luca  
; APPLICANT: Kekuda, Ramesh  
; APPLICANT: Guo, Xiaojia  
; APPLICANT: Zerhusen, Bryan  
; APPLICANT: Andrew, David  
; APPLICANT: Mezes, Peter  
; APPLICANT: Patturajan, Meera  
; APPLICANT: Burgess, Catherine  
; APPLICANT: Eisen, Andrew  
; APPLICANT: Wolenc, Adam  
; APPLICANT: Baumgartner, Jason  
; APPLICANT: Shimketa, Richard  
; APPLICANT: Gusev, Vladimir  
; APPLICANT: Vernet, Corine  
; APPLICANT: Taupier Jr., Raymond  
; APPLICANT: Pena, Carol  
; APPLICANT: Shenoy, Suresh  
; APPLICANT: Li, Li  
; APPLICANT: Casman, Stacie  
; APPLICANT: Boldog, Florence  
; TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoded Thereby  
; FILE REFERENCE: 21402-251  
; CURRENT APPLICATION NUMBER: US/10/055,877  
; CURRENT FILING DATE: 2002-01-22  
; PRIOR APPLICATION NUMBER: 60/262,892  
; PRIOR FILING DATE: 2001-01-19  
; PRIOR APPLICATION NUMBER: 60/263,598  
; PRIOR FILING DATE: 2001-01-23  
; PRIOR APPLICATION NUMBER: 60/263,799  
; PRIOR FILING DATE: 2001-01-24  
; PRIOR APPLICATION NUMBER: 60/264,117  
; PRIOR FILING DATE: 2001-01-25  
; PRIOR APPLICATION NUMBER: 60/264,139  
; PRIOR FILING DATE: 2001-01-25



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Query Match      20.4%; Score 329.5; DB 6; Length 254;
Best Local Similarity 33.7%; Fred. NO. 9.5e-25;
Matches 91; Conservative 54; Mismatches 88; Indels 37; Gaps 9

Qy 28 GVLIVLGLLLNSLALWVFCRQQQTETRIYMTNLAVADLCILCTL-PFVLHSLRD--- 83
||||| :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|:
db 1 GNIAIVILVILTKKI-----RTPTNIFLLNLAVADLCFLTLTPWALYLVGGDWV 51

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US-10-877-346-83

Query Match 20.4%; Score 329.5; DB 6; Length 254;  
Best Local Similarity 33.7%; Pred. No. 9.5e-25;  
Matches 91; Conservative 54; Mismatches 88; Indels 37; Gaps 9;

QY 28 GVLLVGLGLLSLALVFCRCMQQTETRYMTNLAVADCLLCTL-PFVLSLRD---T 83  
DB 1 GNLLVTLVTLTKU-----RPTWIFLNLAVADLLFLLPWALYLVGGDWV 51  
QY 84 SDTFLCQLSQGIYLTNRYSISLVTAIAVDVAVVRHPLRARGLSPROAAAACAVLWVL 143  
DB 52 PGDALCKLVGALFVNGYASILLTAISIDRIAIVHPLRYRIRTPRAKVLILLVWL 111  
QY 144 V-----IGSLVARWLLGIQEGG-----FCFSTRHNFNSMFPPLLGFLYPLAVVVFCSL 192  
DB 112 ALLSLPPLFLSWLRVTVEGNTVCLIDFPESVKRSY-VLLSTLVGFVPLLVILVCVT 170  
QY 193 KVVTAQAQPPDVG---QAEATRKAKRMVANLLVVFVCPFLPHVGLTVRLAVGNACA 249  
DB 171 RLRLTKRKARSORSKRSSSRKAARKMLLVVVVFLCWLPLFYHIVLL-----DSL 224  
QY 250 LLETIR---RALYITSKLSDANCCDAICY 276  
DB 225 LLSIRVLPALLITLWLVNLSCLNPIY 254

RESULT 5

US-11-157-930-2  
; Sequence 2, Application US/11157930  
; Publication No. US20050266482A1  
; GENERAL INFORMATION:  
; APPLICANT: Xieo, Yonghong  
; TITLE OF INVENTION: Regulation of Human CysLT2-Like GPCR  
; FILE REFERENCE: 04974.00458  
; CURRENT APPLICATION NUMBER: US/11/157,930  
; PRIOR FILING DATE: 2005-06-22  
; PRIOR APPLICATION NUMBER: US/09/828,478  
; PRIOR FILING DATE: 2001-04-09  
; PRIOR APPLICATION NUMBER: 60/195,196  
; PRIOR FILING DATE: 2000-04-07  
; PRIOR APPLICATION NUMBER: 60/254,876  
; PRIOR FILING DATE: 2000-12-13  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 346  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-157-930-2

Query Match 19.6%; Score 316.5; DB 7; Length 346;  
Best Local Similarity 28.4%; Pred. No. 2.4e-23;  
Matches 89; Conservative 64; Mismatches 139; Indels 21; Gaps 10;

QY 2 NGTYTCGSSDLTPPAIKGY--AYGLVGLVGLLSLALVFCRCMQQTETRYM 59  
DB 20 NOTFSNNRNCT-IENPKREFPIVYL-IFFWGLVGLNGLSIYVFLQPKKSTSVNVM 77  
QY 60 TNLAVADCLLCTLPF-VLHSLRDS----DFPLCQLSQGIYLTNRYSISLVTAIAVDR 114  
DB 78 LNLASDLLFISTLPFRADYLRGNSWIFGDIACRIMSYSLXV-NMYSSIYFLTVLSVR 136  
QY 115 YVAVRHPLRARGLSRPROAAAACAVLWLVIGSLVARWLLGIQEGG---FCFSTRHNFN 171  
DB 137 FLAWVHPFLHVTIRSAMWICGIIWILIMASSMLLDSGSGVSTSCLEMLNYKIA 196  
QY 172 SMRFP-----LLGFLYPLAVVVFCSLKVVTALAQAQPPDVGQAEATRKAKRMVANLLV 226  
DB 197 KLOTWNYIALVVGCLLPFTLSICVLLIIRVLKVEPESGLRVSHRKALITIIITLIIF 256  
QY 227 VVCFPLPHVGLTVRLAVGNACALLETIRRALYITSKLSDANCCDAICYMAKEPQB- 285

Db 257 FLCFLPYHTLRTVHLTT-WKVGCLCKRLHKAIVTLALAAANACFNPLLYTFAGENFKDR 315  
QY 286 -ASALAVAPRAKA 297  
DB 316 LKSALRKGHPOKA 328

RESULT 6  
US-10-995-561-545  
; Sequence 545, Application US/10995561  
; Publication No. US20050272054A1  
; GENERAL INFORMATION:  
; APPLICANT: CARGILL, Michele et al.  
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF  
; TITLE OF INVENTION: DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001559  
; CURRENT APPLICATION NUMBER: US/10/995,561  
; CURRENT FILING DATE: 2004-11-24  
; NUMBER OF SEQ ID NOS: 85702  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 545  
; LENGTH: 365  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-995-561-545

Query Match 19.5%; Score 315.5; DB 6; Length 365;  
Best Local Similarity 29.2%; Pred. No. 3.2e-23;  
Matches 94; Conservative 56; Mismatches 123; Indels 49; Gaps 12;

QY 29 VLLVGLGLLSLALVFCRCMQQTETRYMTNLAVADCLLCTLPFVLSLRDTSPT- 87  
DB 44 VVFLVGLGLNAPTLWLFIFRLRPWDATATYMFHLASDTLVLSLPTLIYYAAHNPFP 103  
QY 88 ---LCQLSQGIYLTNRYSISLVTAIAVDVAVVRHPLRARGLSRPROAAAACAVLWVLV 144  
DB 104 GTEICKFVRFLFYWNLYCIVLFTCISVHYLGICHPRLRWRGRPRLAGLLCLAVLWV 163  
QY 145 IGSILVAR-WLIGIQEGG---PCFSTR-----H--NFSNMFPLLGFLYPLAVVVFCSLK 193  
DB 164 AGCLVNLFFVTTNSKGTIVLCHDTTPEEDPHVHFSAVMGLL-FGVPCLVTLVCVGL 222  
QY 194 VVTAQAQPPDVGQAEATRKAK--RMVWNLVVFVVCFLPLHYGLTV----RLAVGNNA 247  
DB 223 MARRLYQPLP---GSAQSSSLRLSLRTIAVVLTVFAVCFVPHITRTIYYLARLEA--D 277  
QY 248 CALLETIRRALYITSKLSDANCCDAICYMAKEPQB-----ASALAV 291  
DB 278 CRVLNVVNVVYKVRPLASANSCLDPVLYLTGDKYRRQLRQLCGGKGPQPRTAASSLAL 337  
QY 292 APRAK-----AHKSQSLCVT 307  
DB 338 VSLPEDSSCRWAATPDSSCST 359

RESULT 7

US-11-127-877-52  
; Sequence 52, Application US/11127877  
; Publication No. US20050287565A1  
; GENERAL INFORMATION:  
; APPLICANT: Merckhans, Pascal G.  
; APPLICANT: Hoffmann, Marcel  
; APPLICANT: Spittaels, Koenraad P. P.  
; APPLICANT: Laenen, Wendy  
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting  
; TITLE OF INVENTION: Amyloid-Beta Protein Production  
; FILE REFERENCE: P27,800-B USA  
; CURRENT APPLICATION NUMBER: US/11/127,877  
; CURRENT FILING DATE: 2005-05-12  
; PRIOR APPLICATION NUMBER: 60/570,352  
; PRIOR FILING DATE: 2004-05-12



```

; PRIOR APPLICATION NUMBER: 60/603,948
; PRIOR FILING DATE: 2004-08-24
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 52
; LENGTH: 391
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-127-877-52

Query Match      19.3%; Score 311.5; DB 7; Length 391;
Best Local Similarity 27.6%; Pred. No. 8.3e-23;
Matches 89; Conservative 54; Mismatches 128; Indels 51; Gaps 9;

Qy 1 MNGTYNTCGSDLTW-----PPAKLGFYAVLGVLLVGLLNSLALWVFCRQQW 52
Db 38 LMGTFQSKCPQVEMGLWNTIQPP-----FLWLVFLVATDENFVLSVFCMHKSSC 89

Qy 53 TETRIYMTNLAVADCLLCTLPFVLHSLRDTSD----TPLCQLSQGIYLTNRYSISLVT 108
Db 90 TVAEIYIGNLAADLILACGLPFWAITISNFDWLFGETLCRVVNAISMNLYSSICFLM 149

Qy 109 AIAVDYVAVRHLRLRGLRSPROAAVCAVLW--VLVIGS--LVARWLLGIOGGFCFR 164
Db 150 LVSIDRYLALVKTWSMGRGVRWAKLYSLVINGCTLLSSPMLVFRMTKEYSDEG--- 205

Qy 165 STRIN-----PNSMRFPPLGFLYPLAVVVFCSLKVVTALAQRPTDVGOA 209
Db 206 ---HNVTA CVISPLIWEVETNMLNVLVGVFLPLSVITFCTMQIMQVLRNEMQKPKFI 262

Qy 210 EATRKAKRWYANLLVVFVCPFLPLHVLTV---RLAGWNACALLETTIRRALYITSKLS 265
Db 263 QTRRATVVLVVLVLLFFLICMLPFOISTFTDLTLRLGI-LSSQDERIIDVITQJASFMA 321

Qy 266 DANCCLDAICYNNMAKFEQAS 287
Db 322 YSNSCLNPLVTVIVGKFRKKS 343

RESULT 8
US-10-055-877-225
; Sequence 225, Application US/10055877
; Publication No. US20050288241A1
; GENERAL INFORMATION:
; APPLICANT: DeCristofaro, Marc
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Miller, Charles
; APPLICANT: Tchernev, Velizar
; APPLICANT: Zhong, Mei
; APPLICANT: Anderson, David
; APPLICANT: Ballinger, Robert
; APPLICANT: Gerlach, Valerie
; APPLICANT: Spytek, Kimberly
; APPLICANT: Ratelli, Luca
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Guo, Xiaojia
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Andrew, David
; APPLICANT: Mezes, Peter
; APPLICANT: Patturajan, Meera
; APPLICANT: Burgess, Catherine
; APPLICANT: Eisen, Andrew
; APPLICANT: Wolenc, Adam
; APPLICANT: Baumgartner, Jason
; APPLICANT: Shinkets, Richard
; APPLICANT: Gusev, Vladimir
; APPLICANT: Vernet, Corine
; APPLICANT: Taupier Jr., Raymond
; APPLICANT: Pena, Carol
; APPLICANT: Shenoy, Suresh
; APPLICANT: Li, Li
; APPLICANT: Casman, Stacie
; APPLICANT: Boldog, Ference

; TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoded Thereby
; FILE REFERENCE: 21402-251
; CURRENT APPLICATION NUMBER: US/10/055,877
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: 60/262,892
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: 60/263,598
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 60/263,799
; PRIOR FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: 60/264,117
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/264,139
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/264,478
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/263,351
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/272,870
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 60/275,990
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/275,927
; PRIOR FILING DATE: 2001-03-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 512
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 225
; LENGTH: 259
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: 7tm_1 domain
; OTHER INFORMATION: consensus sequence
US-10-055-877-225

Query Match      18.6%; Score 300; DB 6; Length 259;
Best Local Similarity 32.6%; Pred. No. 6.8e-22;
Matches 92; Conservative 49; Mismatches 85; Indels 56; Gaps 10;

Qy 28 GVLVLGGLLNSLALWVFCRQQWQWETRIYMTNLAVADCLLCTLPFVLHSLRDTSD- 85
Db 1 GNLVLVLVILRTKKL-----RTPTNFIPLNLAVALDELFLTLPPWALYLYVGSGS 51

Qy 86 ----TPLCQLSQGIYLTNRYSISLVTAVAVRHLRLRGLR--SPROAAVCAVL 140
Db 52 WPFGLSALCKLVTDVDDVVMVNASILLTAISIDRYLAVHPLRYRRRTSPRAKVILLV 111

Qy 141 WVLV----IGSLVARWLLGIOGG-----FCFRSTRHNFNSMR-----FPLL 178
Db 112 WVLALLSLPPLFLFSWKVTEEGNGTLNVNVTVCLIDFPBESSTASVSTWLSYVLLSTLV 171

Qy 179 GFYLPVAVVFCSLKVVTALAQRPTDVGOAEATRKAKRWYANLLVVFVCFPLHVLGL- 237
Db 172 GFLLPLVILVCYTRILRTL-----RKAATLLVWVWVFLVCLWLPFYVILL 217

Qy 238 --TVRLAVGWNACALLETTIRRALYITSKLSDANCCLDAICY 276
Db 218 LDTLCLSIIMSSTCELSERVLPFTALLVTLWLAIVVNSCLNPIIY 259

RESULT 9
US-10-055-877-237
; Sequence 237, Application US/10055877
; Publication No. US20050288241A1
; GENERAL INFORMATION:
; APPLICANT: DeCristofaro, Marc
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Miller, Charles
; APPLICANT: Tchernev, Velizar
; APPLICANT: Zhong, Mei
; APPLICANT: Anderson, David
; APPLICANT: Ballinger, Robert
```



|  |     |              |  |     |     |     |     |     |     |
|--|-----|--------------|--|-----|-----|-----|-----|-----|-----|
| CURRENT APPLICATION NUMBER: US/11/157,930                                    |     |              |  |     |     |     |     |     |     |
| CURRENT FILING DATE: 2005-06-22  |     |              |  |     |     |     |     |     |     |
| BEST LOCAL SIMILARITY 29.1%; Pred. No. 1.6e-21;                              |     |              |  |     |     |     |     |     |     |
| Matches 88; Conservative 54; Mismatches 128; Indels 32; Gaps 8;              |     |              |  |     |     |     |     |     |     |
| PRIOR APPLICATION NUMBER: US/09/828,478                                      |     |              |  |     |     |     |     |     |     |
| PRIOR FILING DATE: 2001-04-09  |     |              |  |     |     |     |     |     |     |
| PRIOR APPLICATION NUMBER: 60/195,196   |     |              |  |     |     |     |     |     |     |
| PRIOR FILING DATE: 2000-04-07  |     |              |  |     |     |     |     |     |     |
| PRIOR APPLICATION NUMBER: 60/254,876   |     |              |  |     |     |     |     |     |     |
| PRIOR FILING DATE: 2000-12-13  |     |              |  |     |     |     |     |     |     |
| NUMBER OF SEQ ID NOS: 16   |     |              |  |     |     |     |     |     |     |
| SOFTWARE: FASTSEQ for Windows Version 4.0                                    |     |              |  |     |     |     |     |     |     |
| SEQ ID NO 6  |     |              |  |     |     |     |     |     |     |
| LENGTH: 367  |     |              |  |     |     |     |     |     |     |
| TYPE: PRT  |     |              |  |     |     |     |     |     |     |
| ORGANISM: Homo sapiens   |     |              |  |     |     |     |     |     |     |
| US-11-157-930-6  |     |              |  |     |     |     |     |     |     |
| Query Match 18.5%; Score 298; DB 7; Length 367;                              |     |              |  |     |     |     |     |     |     |
| Best Local Similarity 29.1%; Pred. No. 1.6e-21;                              |     |              |  |     |     |     |     |     |     |
| Matches 88; Conservative 54; Mismatches 128; Indels 32; Gaps 8;              |     |              |  |     |     |     |     |     |     |
| Qy   | 4   | TNTCGSSDLTWP | PAIKLGFVAYLGVLLVGLLNSLALWVFCRMOQWTETRIYMT          | 163 | 103 | 103 | 103 | 103 | 103 |
| Db   | 47  | TAEQCGQE---- | TEPLENMFASPTLLDFILAVGNTLALWLFIRDHSGTTPANVFLMHLA    | 102 | 103 | 103 | 103 | 103 | 103 |
| Qy   | 64  | VADICLLCTLP  | FFVLSLSDTSL-----COLSQGIYLTNRYMSISLVTAIAVDYVAVR     | 119 | 103 | 103 | 103 | 103 | 103 |
| Db   | 103 | VADUSCVLVL   | PTLVYHFGNHPFGEIACRLTGFLFYLNMYASIIYPLTCTISADRFLAIV  | 162 | 103 | 103 | 103 | 103 | 103 |
| Qy   | 120 | HPLRARGLS    | PROAAACAVLWLVIGS-----LVARMLLGIQEGGFCF-----RSTRHNF  | 170 | 103 | 103 | 103 | 103 | 103 |
| Db   | 163 | HPVSKLRLR    | PLXLAHLACAFLVVVAVAMAPLLVSPQVTQNTHTVCLQLYREKASHAL   | 222 | 103 | 103 | 103 | 103 | 103 |
| Qy   | 171 | NSMRFPPL     | GLFVPLAVVVFCSLKVTAIAQRPTDVG---QAEATRKAKRMWANLVFV   | 227 | 103 | 103 | 103 | 103 | 103 |
| Db   | 223 | VSL----      | AVAFPTPTITVTCYLLIIRSLQ-----GLRVEKRLKTRKAVRMIAVLAI  | 273 | 103 | 103 | 103 | 103 | 103 |
| Qy   | 228 | VCFLPLHVL    | TV---RLAVGNACALLETIRRALYITSKLDANCCCLDAICYVMKEFQ    | 284 | 103 | 103 | 103 | 103 | 103 |
| Db   | 274 | VCFPYHVNR    | SVYVLYHVRSHGASCATORILANRITSLTSLNGALDPIIMFFVAEKFR   | 333 | 103 | 103 | 103 | 103 | 103 |
| Qy   | 285 | EA           | 286  |     | 103 | 103 | 103 | 103 | 103 |
| Db   | 334 | HA           | 335  |     | 103 | 103 | 103 | 103 | 103 |
| RESULT 12  |     |              |  |     |     |     |     |     |     |
| US-11-127-877-66   |     |              |  |     |     |     |     |     |     |
| Sequence 66, Application US/11/127877  |     |              |  |     |     |     |     |     |     |
| Publication No. US20050287565A1  |     |              |  |     |     |     |     |     |     |
| GENERAL INFORMATION:   |     |              |  |     |     |     |     |     |     |
| APPLICANT: Merck, Pascal G.  |     |              |  |     |     |     |     |     |     |
| APPLICANT: Hoffmann, Marcel  |     |              |  |     |     |     |     |     |     |
| APPLICANT: Laenen, Wendy   |     |              |  |     |     |     |     |     |     |
| TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting |     |              |  |     |     |     |     |     |     |
| FILE REFERENCE: P27,800-B USA  |     |              |  |     |     |     |     |     |     |
| CURRENT APPLICATION NUMBER: US/11/127,877                                    |     |              |  |     |     |     |     |     |     |
| CURRENT FILING DATE: 2005-05-12  |     |              |  |     |     |     |     |     |     |
| PRIOR APPLICATION NUMBER: 60/570,352   |     |              |  |     |     |     |     |     |     |
| PRIOR FILING DATE: 2004-05-12  |     |              |  |     |     |     |     |     |     |
| PRIOR APPLICATION NUMBER: 60/603,948   |     |              |  |     |     |     |     |     |     |
| PRIOR FILING DATE: 2004-08-24  |     |              |  |     |     |     |     |     |     |
| NUMBER OF SEQ ID NOS: 590  |     |              |  |     |     |     |     |     |     |
| SOFTWARE: PatentIn version 3.3   |     |              |  |     |     |     |     |     |     |
| SEQ ID NO 66   |     |              |  |     |     |     |     |     |     |
| LENGTH: 373  |     |              |  |     |     |     |     |     |     |
| TYPE: PRT  |     |              |  |     |     |     |     |     |     |
| ORGANISM: Homo sapiens   |     |              |  |     |     |     |     |     |     |
| US-11-127-877-46   |     |              |  |     |     |     |     |     |     |
| Query Match 18.4%; Score 296.5; DB 7; Length 373;                            |     |              |  |     |     |     |     |     |     |
| Best Local Similarity 26.2%; Pred. No. 2.2e-21;                              |     |              |  |     |     |     |     |     |     |
| Matches 88; Conservative 72; Mismatches 137; Indels 39; Gaps 10;             |     |              |  |     |     |     |     |     |     |
| Qy   | 3   | GTNTCGSSDLT  | WPAPAI-----KLGF-YAYLG-----VLLVGLLNSLALWVFCR        | 48  | 103 | 103 | 103 | 103 | 103 |
| Db   | 20  | GPSSGNGST    | VASTAAVSSPFKALTKTGFYVILPAVYVILFIIGLNSVAINWVPH      | 79  | 103 | 103 | 103 | 103 | 103 |
| Qy   | 49  | MOQWTETRIY   | MNLAVADLCCLTLPFVLSLSDTSD----TPLCQLSQGIYLTNRYMSI    | 104 | 103 | 103 | 103 | 103 | 103 |
| Db   | 80  | MKPMGSI      | YVFNALADFLVLTLPALIFYYFNKTDWIFGDMCKLQRFIFHVLNLSI    | 139 | 103 | 103 | 103 | 103 | 103 |
| Qy   | 105 | SLVTAIAVD    | RYVVRHPLRARGLSPROAAACAVLWLV---IGSLVARMLLGIQEGG-    | 160 | 103 | 103 | 103 | 103 | 103 |
| Db   | 140 | LPLTCTISA    | HRYSGVVYPLKSLGRLKKNAICISLVWLVVVAISPILFYSYSGTVRKNKT | 199 | 103 | 103 | 103 | 103 | 103 |
| Qy   | 161 | -FCFSTRHNF   | -----NSMRFPPLGLFVPLAVVVFCSLKVTAIAQRPTDVGQAEATR     | 213 | 103 | 103 | 103 | 103 | 103 |
| Db   | 200 | ITCYDTTSD    | EVLSRYFIYSMCTTAMFCVPLVILGCGYGLIVRALIYK---DLN       | 256 | 103 | 103 | 103 | 103 | 103 |



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OM protein - protein search, using sw model

Run on: February 9, 2006, 01:16:44 ; Search time 118.5 Seconds  
(without alignments)  
1089.530 Million cell updates/sec

Title: US-10-083-168-16

Perfect score: 1614

Sequence: 1 MNGTYNTCGSSDLTPPAIK.....AVAPRAKAHKSQDSLCVTLA 309

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main:\*

1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*  
2: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*  
3: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep.\*  
4: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*  
5: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*  
6: /cgn2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query Match % | Length | ID                   | Description       |
|------------|-------|---------------|--------|----------------------|-------------------|
| 1          | 1614  | 100.0         | 309    | 3 US-09-768-877-20   | Sequence 20, Appl |
| 2          | 1614  | 100.0         | 309    | 4 US-10-225-567A-492 | Sequence 492, App |
| 3          | 1614  | 100.0         | 309    | 5 US-10-696-639-44   | Sequence 44, Appl |
| 4          | 1608  | 99.6          | 547    | 5 US-10-505-486-84   | Sequence 84, Appl |
| 5          | 1602  | 99.3          | 309    | 4 US-10-157-031-351  | Sequence 351, App |
| 6          | 402   | 24.9          | 370    | 3 US-09-964-821B-11  | Sequence 11, Appl |
| 7          | 402   | 24.9          | 370    | 4 US-10-081-810-44   | Sequence 44, Appl |
| 8          | 402   | 24.9          | 370    | 4 US-10-225-567A-225 | Sequence 225, App |
| 9          | 402   | 24.9          | 370    | 4 US-10-024-298A-176 | Sequence 176, App |
| 10         | 402   | 24.9          | 370    | 4 US-10-042-211A-176 | Sequence 176, App |
| 11         | 402   | 24.9          | 370    | 4 US-10-268-332-11   | Sequence 11, Appl |
| 12         | 402   | 24.9          | 370    | 4 US-10-617-217A-176 | Sequence 176, App |
| 13         | 402   | 24.9          | 370    | 4 US-10-775-965-11   | Sequence 11, Appl |
| 14         | 402   | 24.9          | 370    | 4 US-10-024-298A-176 | Sequence 176, App |
| 15         | 402   | 24.9          | 370    | 5 US-10-753-267-86   | Sequence 86, Appl |
| 16         | 402   | 24.9          | 608    | 5 US-10-505-486-114  | Sequence 114, App |
| 17         | 401   | 24.8          | 370    | 3 US-09-964-821B-10  | Sequence 10, Appl |
| 18         | 401   | 24.8          | 370    | 4 US-10-268-332-10   | Sequence 10, Appl |
| 19         | 392   | 24.3          | 370    | 4 US-10-024-298A-174 | Sequence 174, App |
| 20         | 392   | 24.3          | 370    | 4 US-10-042-211A-174 | Sequence 174, App |
| 21         | 392   | 24.3          | 370    | 4 US-10-617-217A-174 | Sequence 174, App |
| 22         | 392   | 24.3          | 370    | 4 US-10-024-298A-174 | Sequence 174, App |
| 23         | 390   | 24.2          | 368    | 4 US-10-775-965-10   | Sequence 10, Appl |
| 24         | 381.5 | 23.6          | 363    | 4 US-10-314-048A-159 | Sequence 159, App |
| 25         | 381.5 | 23.6          | 363    | 5 US-10-897-815-159  | Sequence 159, App |
| 26         | 381.5 | 23.6          | 363    | 5 US-10-930-662-159  | Sequence 159, App |
| 27         | 376.5 | 23.3          | 363    | 3 US-09-930-334-16   | Sequence 16, Appl |

## ALIGNMENTS

### RESULT 1

US-09-768-877-20  
; Sequence 20, Application US/09768877  
; Patent No. US20020150896A1  
; GENERAL INFORMATION:  
; APPLICANT: POLONSKY, KENNETH S.  
; APPLICANT: HORIKAWA, YUKIO  
; APPLICANT: ODA, NAOHISA  
; APPLICANT: COX, NANCY J.  
; APPLICANT: SREENAN, SEAMUS  
; APPLICANT: ZHOU, YUN-PING  
; APPLICANT: OTANI, KENICHI  
; APPLICANT: HANIS, CRAIG L.  
; APPLICANT: BELL, GRAEME I.  
; TITLE OF INVENTION: METHODS OF TREATMENT OF TYPE 2 DIABETES  
; FILE REFERENCE: ARCD:307  
; CURRENT APPLICATION NUMBER: US/09/768, 877  
; CURRENT FILING DATE: 2001-01-23  
; PRIOR APPLICATION NUMBER: 09/422, 869  
; PRIOR FILING DATE: 1999-10-21  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 20  
; LENGTH: 309  
; TYPE: PRT  
; ORGANISM: Human  
US-09-768-877-20

Query Match 100.0%; Score 1614; DB 3; Length 309;

Best Local Similarity 100.0%; Pred. No. 1.2e-145; Indels 0; Gaps 0;  
Matches 309; Conservative 0; Mismatches 0;

|    |     |   |     |
|----|-----|---|-----|
| QY | 1   | MNGTYNTCGSSDLTPPAIKLGFYALGVLLVGLLLNSLALWFCCRMQQQTETRIYMT  | 60  |
| DB | 1   | MNGTYNTCGSSDLTPPAIKLGFYALGVLLVGLLLNSLALWFCCRMQQQTETRIYMT  | 60  |
| QY | 61  | NLAVALDCLLCTLPFVLSLRDTSPTPLCQLSQGYLTNRNYSISLVTIAVDYVAVRH  | 120 |
| DB | 61  | NLAVALDCLLCTLPFVLSLRDTSPTPLCQLSQGYLTNRNYSISLVTIAVDYVAVRH  | 120 |
| QY | 121 | PLRAGRLSPROAAVCAVLVLTGSLVARMLLQEGGFCFRSTRHFNNSMRFPLLGF    | 180 |
| DB | 121 | PLRAGRLSPROAAVCAVLVLTGSLVARMLLQEGGFCFRSTRHFNNSMRFPLLGF    | 180 |
| QY | 181 | YLPLAVVFCSLKVVTALAQRPPTDVGQAEATKAAWYMANLLVFVVCFLPLHVLGTVR | 240 |
| DB | 181 | YLPLAVVFCSLKVVTALAQRPPTDVGQAEATKAAWYMANLLVFVVCFLPLHVLGTVR | 240 |
| QY | 241 | LAVGWNCALLETIRREALYITSKLSDANCLDAICYNYMAKEFQEASALAVAPRAKHS | 300 |
| DB | 241 | LAVGWNCALLETIRREALYITSKLSDANCLDAICYNYMAKEFQEASALAVAPRAKHS | 300 |

Sequence 16, Appl  
Sequence 1, Appl  
Sequence 4, Appl  
Sequence 54202, A  
Sequence 45, Appl  
Sequence 36, Appl  
Sequence 226, App  
Sequence 668, App  
Sequence 36, Appl  
Sequence 36, Appl  
Sequence 14, Appl  
Sequence 36, Appl  
Sequence 4, Appl  
Sequence 766, App  
Sequence 2, Appl  
Sequence 808, App  
Sequence 12, Appl

28 376.5 23.3 363 4 US-10-619-141-16  
29 376 23.3 319 4 US-10-167-192-1  
30 376 23.3 319 4 US-10-400-991-4  
31 376 23.3 383 5 US-10-450-763-54202  
32 376 23.3 557 5 US-10-505-486-45  
33 375.5 23.3 363 4 US-10-321-807-36  
34 375.5 23.3 363 4 US-10-295-027-226  
35 375.5 23.3 363 4 US-10-292-798-668  
36 375.5 23.3 363 4 US-10-321-807-36  
37 375.5 23.3 363 4 US-10-314-048A-36  
38 375.5 23.3 363 5 US-10-484-788-14  
39 375.5 23.3 363 5 US-10-897-815-36  
40 375.5 23.3 363 5 US-10-930-662-36  
41 375.5 23.3 363 5 US-10-800-249-4  
42 375.5 23.3 364 4 US-10-017-161-766  
43 375.5 23.3 387 5 US-10-800-249-2  
44 375.5 23.3 392 4 US-10-017-161-808  
45 371.5 23.0 363 5 US-10-484-788-12

|    |     |        |          |         |         |         |      |       |       |      |     |
|----|-----|--------|----------|---------|---------|---------|------|-------|-------|------|-----|
| Db | 241 | LAGWNA | LETIRRAL | YITSKLS | DANCCLD | DAICYYM | AKFQ | EASAL | VAPRA | KAHS | 300 |
| Qy | 301 | QDSL   | CVTLA    | 309     |         |         |      |       |       |      |     |
| Db | 301 | QDSL   | CVTLA    | 309     |         |         |      |       |       |      |     |

## RESULT 2

US-10-225-567A-492  
; Sequence 492, Application US/10225567A  
; Publication No. US20030113798A1  
; GENERAL INFORMATION:  
; APPLICANT: LifeSpan Biosciences  
; APPLICANT: Brown, Joseph P.  
; APPLICANT: Burner, Glenn C.  
; APPLICANT: Roush, Christine L.  
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS  
; FILE REFERENCE: 1920-4-4  
; CURRENT APPLICATION NUMBER: US/10/225,567A  
; CURRENT FILING DATE: 2001-12-19  
; PRIOR APPLICATION NUMBER: 60/257,144  
; PRIOR FILING DATE: 2000-12-19  
; NUMBER OF SEQ ID NOS: 2292  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 492  
; LENGTH: 309  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-225-567A-492

```
Query Match      100.0%; Score 1614; DB 4; Length 309;
Best Local Similarity 100.0%; Pred. No. 1.2e-145;
Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

[illegible][illegible]

Qy 121 PLRARGLRSPQAAAACAVLWVLVTGSLVARWLLGIQEGGFCFRSTRHNFNSMRPFLIGF 180  
|||  
Db 121 PLRARGLRSPQAAAACAVLWVLVTGSLVARWLLGIQEGGFCFRSTRHNFNSMRPFLIGF 180

[illegible][illegible]

Qy 301 QDSLCTTLLA 309

Dh 301 QDSLCTTLLA 309

### RESULT 3

```

RES001 3
US-10-696-639-44
; Sequence 44, Application US/10696639
; Publication No. US20050037439A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corporation
; APPLICANT: Bourner, Maureen J.
; TITLE OF INVENTION: DIFFERENTIALLY EXPRESSED GENES INVOLVED IN CANCER, THE
; TITLE OF INVENTION: POLYPEPTIDES ENCODED THEREBY, AND METHODS OF USING THE SAME
; FILE REFERENCE: 01040/1
; CURRENT APPLICATION NUMBER: US/10/696,639
; CURRENT FILING DATE: 2003-10-29
; PRIOR APPLICATION NUMBER: 60/422,176
; PRIOR FILING DATE: 2002-10-29

```

```

; NUMBER OF SEQ ID NOS: 3114
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 44
; LENGTH: 309
; TYPE: prt
; ORGANISM: homo sapiens
US-0696-639-44

```

|                       |                 |                     |          |             |
|-----------------------|-----------------|---------------------|----------|-------------|
| Query Match           | 100.0%          | Score 1614;         | DB 5;    | Length 309; |
| Best Local Similarity | 100.0%;         | Pred. NO. 1.2e-145; |          |             |
| Matches 309;          | Conservative 0; | Mismatches 0;       | Indels 0 |             |

|                      |  |
|----------------------|--|
| <b>Qy</b>            | <pre> 1 MNGTYNTCGSSDLTWPPAIKGFYAYLVLLVGLLNSLAIVFCCRMQQTETRIYMT 60       </pre> |
| <b>D<sub>b</sub></b> | <pre> 1 MNGTYNTCGSSDLTWPPAIKGFYAYLVLLVGLLNSLAIVFCCRMQQTETRIYMT 60       </pre> |

|    |    |   |     |
|----|----|---|-----|
| Qy | 61 | NLAVADLCILCTTLPVLTSLRDTSDTPLCQLSQGIYLTNPRYMSISLVTAIAVDRYVAVRH | 120 |
| Db | 61 | NLAVADLCILCTTLPVLTSLRDTSDTPLCQLSQGIYLTNPRYMSISLVTAIAVDRYVAVRH | 120 |

Qy 121 PIPARGLRSPROAAACVAVLVLVIGSLVARWLLIGIQEGGFCFRSTRNFNSMRFPLLGF 180

Dh 121 PIPARGLRSPROAAACVAVLVLVIGSLVARWLLIGIQEGGFCFRSPHNFNSMRFDLIGF 180

|    |     |                 |                  |             |              |     |
|----|-----|-----------------|------------------|-------------|--------------|-----|
| Qy | 181 | YPLAVVFCSLKVVTA | LQRPPDVGAEATRKAR | MVWVANLLVFV | VCFLPHVGLTVR | 240 |
| Dh | 191 | YPLAVVFCSLKVVTA | LQRPPDVGAEATRKAR | MVWVANLLVFV | VCFLPHVGLTVR | 240 |

[illegible]

Qy 301 QDSL CVTILA 309  
|||||  
201 0000 0000 0000

## RESULT 4

```

US-10-505-486-84
; Sequence 84, Application US/10505486
; Publication No. US20050118639A1
; GENERAL INFORMATION:
; APPLICANT: Takeda Chemical Industries, Ltd.
; TITLE OF INVENTION: Determination of a ligand
; FILE REFERENCE: P03-0006PCT
; CURRENT APPLICATION NUMBER: US/10/505,486
; CURRENT FILING DATE: 2004-08-20
; PRIOR APPLICATION NUMBER: JP 2002-45728
; PRIOR FILING DATE: 2002-02-22
; PRIOR APPLICATION NUMBER: JP 2002-213949
; PRIOR FILING DATE: 2002-07-23
; PRIOR APPLICATION NUMBER: JP 2002-298237
; PRIOR FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 233
; SEQ ID NO 84
; LENGTH: 547
; TYPE: PRT
; ORGANISM: Human
US-10-505-486-84

```

|                           |       |                     |           |             |
|---------------------------|-------|---------------------|-----------|-------------|
| Query Match               | 99.6% | Score 1608;         | DB 5;     | Length 547; |
| Best Local Similarity     | 99.7% | Pred. No. 8.4e-145; |           |             |
| Matches 308: Conservative | 0;    | Mismatches 1;       | Indels 0; | Gaps 0;     |

Qy 1 MNGTYNTCGSSDITWPPAIKLGFYAYLGVLLVLLGLLNSIALWVPCRMQOWTETRIYMT 60

Dp 1 MNGTYNTCGSSDITWPPAIKLGFYAYLGVLLVLLGLLNSIALWVPCRMQOWTETRIYMT 60

| Qy | 61  | NTAVADLCCLCTTLPFVLHSLRDSDTPLCOLSQGLYLTNRYMSISLVTAIAVDRYVAVRH | 120 |
|----|---|--|-----|
| Dh | 61 <td>NTAVADLCCLCTTLPFVLHSLRDSDTPLCOLSQGLYLTNRYMSISLVTAIAVDRYVAVRH</td> <td>120</td> | NTAVADLCCLCTTLPFVLHSLRDSDTPLCOLSQGLYLTNRYMSISLVTAIAVDRYVAVRH | 120 |

121 PLRARGLSRPROAAA<sup>1</sup>CAVLWVLVIGSLVARWLLGIQEGGFCFRSTRHNFSMRFP<sup>1</sup>LLGF 180

Db 121 PLRARGLSRPRQAAVCAVLVVLVIGSLVWMLLGIQGGCFSTRHNFNSMAFPLLG 180  
Qy 181 YLPLAVVFCSLKVVTALAQRPPTDVQAEATRKAAARMVWNLVVFVCFPLHVGLTVR 240  
Db 181 YLPLAVVFCSLKVVTALAQRPPTDVQAEATRKAAARMVWNLVVFVCFPLHVGLTVR 240  
Qy 241 LAVGNACALLETIRRALYITSKLSDANCCCLDAICYYYMAKEFQASALAVAPRAKAHS 300  
Db 241 LAVGNACALLETIRRALYITSKLSDANCCCLDAICYYYMAKEFQASALAVAPRAKAHS 300  
Qy 301 QDSLVCVTLA 309  
Db 301 QDSLVCVTLA 309

## RESULT 5

US-10-157-031-351  
; Sequence 351, Application US/10157031  
; Publication No. US20030108890A1  
; GENERAL INFORMATION:  
; APPLICANT: Baranova, A. V.  
; APPLICANT: Yankovsky, N. K.  
; APPLICANT: Kozlov, A. P.  
; APPLICANT: Lobashev, A. V.  
; APPLICANT: Krukovskaya, L. L.  
; TITLE OF INVENTION: In silico screening for phenotype-associated expressed sequences  
; FILE REFERENCE: 2760-103  
; CURRENT APPLICATION NUMBER: US/10/157,031  
; PRIOR FILING DATE: 2002-05-30  
; NUMBER OF SEQ ID NOS: 415  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 351  
; LENGTH: 309  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-157-031-351

Query Match 99.3%; Score 1602; DB 4; Length 309;  
Best Local Similarity 99.4%; Pred. No. 1.6e-144;  
Matches 307; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MNGTYNTCGSSDLTPPPAIKLGFIAYLGVLLVGLLNLALWVFCRMOQWTEIRYMT 60  
Db 1 MNGTYNTCGSSDLTPPPAIKLGFIAYLGVLLVGLLNLALWVFCRMOQWTEIRYMT 60  
Qy 61 NLAVADLCLLCTLPFVLSLRTSDTLPCLQSGIYLTNRYSISLVTALVDRYVAVRH 120  
Db 61 NLAVADLCLLCTLPFVLSLRTSDTLPCLQSGIYLTNRYSISLVTALVDRYVAVRH 120  
Qy 121 PLRARGLSRPRQAAVCAVLVVLVIGSLVWMLLGIQGGCFSTRHNFNSMAFPLLG 180  
Db 121 PLRARGLSRPRQAAVCAVLVVLVIGSLVWMLLGIQGGCFSTRHNFNSMAFPLLG 180  
Qy 181 YLPLAVVFCSLKVVTALAQRPPTDVQAEATRKAAARMVWNLVVFVCFPLHVGLTVR 240  
Db 181 YLPLAVVFCSLKVVTALAQRPPTDVQAEATRKAAARMVWNLVVFVCFPLHVGLTVR 240  
Qy 241 LAVGNACALLETIRRALYITSKLSDANCCCLDAICYYYMAKEFQASALAVAPRAKAHS 300  
Db 241 LAVGNACALLETIRRALYITSKLSDANCCCLDAICYYYMAKEFQASALAVAPRAKAHS 300  
Qy 301 QDSLVCVTLA 309  
Db 301 QDSLVCVTLA 309

## RESULT 6

US-09-964-821B-11  
; Sequence 11, Application US/09964821B  
; Publication No. US20030186360A1  
; GENERAL INFORMATION:  
; APPLICANT: FEDER, J. N.

; APPLICANT: MINTIER, G.  
; APPLICANT: RAMANATHAN, C. S.  
; APPLICANT: HAKEN, D.R.  
; APPLICANT: CACACE, A.  
; APPLICANT: BARBER, L.  
; APPLICANT: KORNACKER, M. G.  
; TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPRBMV3,  
; TITLE OF INVENTION: EXPRESSED HIGHLY IN IMMUNE- AND COLON- RELATED TISSUES  
; FILE REFERENCE: D0042NP  
; CURRENT APPLICATION NUMBER: US/09/964,821B  
; CURRENT FILING DATE: 2002-06-10  
; PRIOR APPLICATION NUMBER: 60/235,713  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: 60/261,783  
; PRIOR FILING DATE: 2001-01-17  
; PRIOR APPLICATION NUMBER: 60/305,085  
; PRIOR FILING DATE: 2001-07-13  
; PRIOR APPLICATION NUMBER: 60/313,171  
; PRIOR FILING DATE: 2001-08-17  
; NUMBER OF SEQ ID NOS: 63  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 11  
; LENGTH: 370  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-964-821B-11

Query Match 24.9%; Score 402; DB 3; Length 370;  
Best Local Similarity 34.1%; Pred. No. 8.2e-30;  
Matches 103; Conservative 60; Mismatches 111; Indels 28; Gaps 10;

Qy 25 AVLGVLLVGLLNLALWVFCRMOQWTEIRYMTNLAVADLCLLCTLPF-VLHSLR-- 81  
Db 44 AVSVVFLGLITNSVLSLFCFRMKRSETAFTNLAVSDLLFVCTLPFKIFYNFNRH 103  
Qy 82 -DTSPTPLCQLSQGIYLTNRYSISLVTALVDRYVAVRHPLRARGLSRPRQAAVCAVL 140  
Db 104 WPFQGT-LCKISGTAFTLNIYGSMLFTCISVDRELAIVYPPRSRTIRTRNSAIVCAGV 162  
Qy 141 WVLVIGSLVWMLLGIQGGCFSTRHNFNSMR--FPLLGFLVPLAVVVF 189  
Db 163 WILVSGSISASLSTTNVNNATTCFEGFSKRVWKYLSKTIPIEVVGFIIPLINVS 222  
Qy 190 CSLKVVTALAQRPPTDVQAEAT-RKAAARMVWNLVVFVCFPLHVGLTVRLAVGNAC 248  
Db 223 CSSVVRITL--RKPAITLSQIGTNKKKXLMITVHMAVFCVFPVNSVLFLVALVRSQAI 280  
Qy 249 --ALLETIRRALY-ITSKLSDANCCCLDAICYYYMAKEFQASALAVAPRAKAHSQDSLC 305  
Db 281 TNCFLERPAKIMYPITLCLATLNCDFPFIYVFTLESFQKSFYI-----NAHIRMESLF 334  
Qy 306 VT 307  
Db 335 KT 336

## RESULT 7

US-10-081-810-44  
; Sequence 44, Application US/10081810  
; Publication No. US20030064438A1  
; GENERAL INFORMATION:  
; APPLICANT: Bristol-Myers Squibb Company  
; TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTOR NUCLEIC ACIDS, POLYPEPTIDES, ANTIBODI  
; FILE REFERENCE: D0132 NP  
; CURRENT APPLICATION NUMBER: US/10/081,810  
; CURRENT FILING DATE: 2002-02-22  
; PRIOR APPLICATION NUMBER: US 60/270,793  
; PRIOR FILING DATE: 2001-02-23  
; PRIOR APPLICATION NUMBER: US 60/270,792  
; PRIOR FILING DATE: 2001-02-23  
; PRIOR APPLICATION NUMBER: US 60/296,427  
; PRIOR FILING DATE: 2001-06-06

```
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 44
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-081-810-44

Query Match      24.9%; Score 402; DB 4; Length 370;
Best Local Similarity 34.1%; Pred. No. 8.2e-30;
Matches 103; Conservative 60; Mismatches 111; Indels 28; Gaps 10;

QY 25 AYLGVLVGLLNSLALWFCRMOQWETRIYMTNLAVADICLLCTLPF-VLHSLR-- 81
DB 44 AVYSVVFILGLITNSVSLVFCFRMKRSETAIFITNLAVSDLLFVCTLPFKIFYNFRH 103
QY 82 -DTSDFPLCOLSQGIYLTNRNYSISLVTAIVDRYVAVRHPLRARGLRSPROAAAVCAVL 140
DB 104 WPFQDT-LCKISGTAFITNIYGSMLFLTCISVDRFLAIVYVPSRTIRTRNSAIVCAGV 162
QY 141 WVLVIGSLVARWLLGIQEQ-----GGCFRSTRHNFSMR--PPLIGFYPLAVVVVF 189
DB 163 WILVLSGGISASLFSSTNNVNNATTCFEGFSKRVKMTYLSKITIFIEVVGFIPIILNVS 222
QY 190 CSLKVVTAQAORPPTDVGQAEAT-RKAARMVWNLVVFVCFPLPLHVGTLTVRLAVGMNAC 248
DB 223 CSSVVLRTL--RKPATLSQIGTNKKVKLMITVHMAVVFVCFVYNSVLFYALVRSQAI 280
QY 249 --ALLETIRRALY-ITSKLSDANCCLDALCYIYMAKEFOEASALAVAPRAKAHKSODSLC 305
DB 281 TNCFLERPAKIMYPITCLATLNCDFPFIYFTLESFQKSPYI-----NAHIRMESLF 334
QY 306 VT 307
DB 335 KT 336

RESULT 8
US-10-225-567A-225
; Sequence 225, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burmer, Glenna C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 225
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-225

Query Match      24.9%; Score 402; DB 4; Length 370;
Best Local Similarity 34.1%; Pred. No. 8.2e-30;
Matches 103; Conservative 60; Mismatches 111; Indels 28; Gaps 10;

QY 25 AYLGVLVGLLNSLALWFCRMOQWETRIYMTNLAVADICLLCTLPF-VLHSLR-- 81
DB 44 AVYSVVFILGLITNSVSLVFCFRMKRSETAIFITNLAVSDLLFVCTLPFKIFYNFRH 103
QY 82 -DTSDFPLCOLSQGIYLTNRNYSISLVTAIVDRYVAVRHPLRARGLRSPROAAAVCAVL 140
DB 104 WPFQDT-LCKISGTAFITNIYGSMLFLTCISVDRFLAIVYVPSRTIRTRNSAIVCAGV 162
QY 141 WVLVIGSLVARWLLGIQEQ-----GGCFRSTRHNFSMR--PPLIGFYPLAVVVVF 189
DB 163 WILVLSGGISASLFSSTNNVNNATTCFEGFSKRVKMTYLSKITIFIEVVGFIPIILNVS 222
QY 190 CSLKVVTAQAORPPTDVGQAEAT-RKAARMVWNLVVFVCFPLPLHVGTLTVRLAVGMNAC 248
DB 223 CSSVVLRTL--RKPATLSQIGTNKKVKLMITVHMAVVFVCFVYNSVLFYALVRSQAI 280
QY 249 --ALLETIRRALY-ITSKLSDANCCLDALCYIYMAKEFOEASALAVAPRAKAHKSODSLC 305
DB 281 TNCFLERPAKIMYPITCLATLNCDFPFIYFTLESFQKSPYI-----NAHIRMESLF 334
QY 306 VT 307
DB 335 KT 336

RESULT 9
US-10-024-298A-176
; Sequence 176, Application US/10024298A
; Publication No. US20030143540A1
; GENERAL INFORMATION:
; APPLICANT: ASAHI KASEI KABUSHIKI KAISHA
; APPLICANT: AKIO MATSUDA
; APPLICANT: GOICHI HONDA
; APPLICANT: SHUJI MURAMATSU
; APPLICANT: YUKIKO NAGANO
; TITLE OF INVENTION: NF-K B Activating Gene
; FILE REFERENCE: 1254-0191P
; CURRENT APPLICATION NUMBER: US/10/024,298A
; CURRENT FILING DATE: 2003-04-08
; PRIOR APPLICATION NUMBER: 60/314,385
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 60/278,641
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: 60/258,315
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: JP254018/2001
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: JP0088912/2001
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: JP402288/2000
; PRIOR FILING DATE: 2000-12-28
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 176
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-024-298A-176

Query Match      24.9%; Score 402; DB 4; Length 370;
Best Local Similarity 34.1%; Pred. No. 8.2e-30;
Matches 103; Conservative 60; Mismatches 111; Indels 28; Gaps 10;

QY 25 AYLGVLVGLLNSLALWFCRMOQWETRIYMTNLAVADICLLCTLPF-VLHSLR-- 81
DB 44 AVYSVVFILGLITNSVSLVFCFRMKRSETAIFITNLAVSDLLFVCTLPFKIFYNFRH 103
QY 82 -DTSDFPLCOLSQGIYLTNRNYSISLVTAIVDRYVAVRHPLRARGLRSPROAAAVCAVL 140
DB 104 WPFQDT-LCKISGTAFITNIYGSMLFLTCISVDRFLAIVYVPSRTIRTRNSAIVCAGV 162
QY 141 WVLVIGSLVARWLLGIQEQ-----GGCFRSTRHNFSMR--PPLIGFYPLAVVVVF 189
DB 163 WILVLSGGISASLFSSTNNVNNATTCFEGFSKRVKMTYLSKITIFIEVVGFIPIILNVS 222
QY 190 CSLKVVTAQAORPPTDVGQAEAT-RKAARMVWNLVVFVCFPLPLHVGTLTVRLAVGMNAC 248
DB 223 CSSVVLRTL--RKPATLSQIGTNKKVKLMITVHMAVVFVCFVYNSVLFYALVRSQAI 280
QY 249 --ALLETIRRALY-ITSKLSDANCCLDALCYIYMAKEFOEASALAVAPRAKAHKSODSLC 305
DB 281 TNCFLERPAKIMYPITCLATLNCDFPFIYFTLESFQKSPYI-----NAHIRMESLF 334
QY 306 VT 307
DB 335 KT 336
```



QY 306 VT 307  
Db 335 KT 336

RESULT 10

US-10-042-211A-176  
; Sequence 176, Application US/10042211A  
; Publication No. US20030170719A1  
; GENERAL INFORMATION:  
; APPLICANT: MATSUDA, Akio et al.  
; TITLE OF INVENTION: NF-kB Activating Gene  
; FILE REFERENCE: 1254-0192P  
; CURRENT APPLICATION NUMBER: US/10/042,211A  
; PRIOR FILING DATE: 2002-01-11  
; PRIOR APPLICATION NUMBER: JP 2000-402288  
; PRIOR FILING DATE: 2000-12-28  
; PRIOR APPLICATION NUMBER: JP 2001-088912  
; PRIOR FILING DATE: 2001-03-26  
; PRIOR APPLICATION NUMBER: JP 2001-254018  
; PRIOR FILING DATE: 2001-08-24  
; PRIOR APPLICATION NUMBER: US 60/258,315  
; PRIOR FILING DATE: 2000-12-28  
; PRIOR APPLICATION NUMBER: US 60/278,640  
; PRIOR FILING DATE: 2001-03-26  
; PRIOR APPLICATION NUMBER: US 60/314,385  
; PRIOR FILING DATE: 2001-08-24  
; NUMBER OF SEQ ID NOS: 182  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 176  
; LENGTH: 370  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-042-211A-176

Query Match 24.9%; Score 402; DB 4; Length 370;

Best Local Similarity 34.1%; Pred. No. 8.2e-30;  
Matches 103; Conservative 60; Mismatches 111; Indels 28; Gaps 10;  
  
QY 25 AYLGVLVGLLNSLALWVFCRQWQWTTETRIYMTNLAVADLCLLCTLPF-VLHSLR-- 81  
Db 44 AVYVVFILGLITNSVLSVFCFRMKRSETAIFITNLAVSDLLFVCTLPFKIFYNFRH 103  
  
QY 82 -DTSPTLCQLSQGIYLTNRYSISLVTAIAVDYVAVRHPRLRGLRSPROAAVCAVL 140  
Db 104 WPFQGT-LCKISGTAFITNIYGSMLFSLTICISVDRLAIVYFPRSTIRTRNSAIVCAGV 162  
  
QY 141 WVLVIGSLVARWLLGIQE-----GGFCFRSTRHNFNSMR--PPLLGFLVPLAVVVF 189  
Db 163 WILVLSGGISASLSTNNVNNATTCFEGFSKRVKTKITIFIEVVGFIPLILNVS 222  
  
QY 190 CSLKVVVTAALQRPPTDVQAEAT-RKAARMVWVANLLVFCVCPFLPHVGLTVRLAYGWNAC 248  
Db 223 CSSVVLRTL--RKATLSQIGTNKKVLMITVHMAVFCVFPVNSVLFVALVRSQAI 280  
  
QY 249 --ALLETIRRALY-ITSKLSANDCCLDACIYYMAKEQOEASALAVAPRAKAKHSQDSLC 305  
Db 281 TNCFLERFAKIMYPITLCLATLNCDFPFIYFTLESFQKSFYI-----NAHIRMESLIF 334  
  
QY 306 VT 307  
Db 335 KT 336

RESULT 11

US-10-268-332-11  
; Sequence 11, Application US/10268332  
; Publication No. US20030175748A1  
; GENERAL INFORMATION:  
; APPLICANT: Bristol-Myers Squibb Company  
; TITLE OF INVENTION: NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPRBMV3, EXPRESSED HIGHLY IN IMMUNE- AND COLON- RELATED TISSUES

; FILE REFERENCE: D0042A CIP  
; CURRENT APPLICATION NUMBER: US/10/268,332  
; CURRENT FILING DATE: 2002-10-10  
; PRIOR APPLICATION NUMBER: U.S. 60/235,713  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: U.S. 60/261,783  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: U.S. 60/305,085  
; PRIOR FILING DATE: 2001-07-13  
; PRIOR APPLICATION NUMBER: U.S. 60/313,171  
; PRIOR FILING DATE: 2001-08-17  
; PRIOR APPLICATION NUMBER: U.S. 09/964,821  
; PRIOR FILING DATE: 2001-09-26  
; NUMBER OF SEQ ID NOS: 66  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 11  
; LENGTH: 370  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-268-332-11

Query Match 24.9%; Score 402; DB 4; Length 370;

Best Local Similarity 34.1%; Pred. No. 8.2e-30;  
Matches 103; Conservative 60; Mismatches 111; Indels 28; Gaps 10;  
  
QY 25 AYLGVLVGLLNSLALWVFCRQWQWTTETRIYMTNLAVADLCLLCTLPF-VLHSLR-- 81  
Db 44 AVYVVFILGLITNSVLSVFCFRMKRSETAIFITNLAVSDLLFVCTLPFKIFYNFRH 103  
  
QY 82 -DTSPTLCQLSQGIYLTNRYSISLVTAIAVDYVAVRHPRLRGLRSPROAAVCAVL 140  
Db 104 WPFQGT-LCKISGTAFITNIYGSMLFSLTICISVDRLAIVYFPRSTIRTRNSAIVCAGV 162  
  
QY 141 WVLVIGSLVARWLLGIQE-----GGFCFRSTRHNFNSMR--PPLLGFLVPLAVVVF 189  
Db 163 WILVLSGGISASLSTNNVNNATTCFEGFSKRVKTKITIFIEVVGFIPLILNVS 222  
  
QY 190 CSLKVVVTAALQRPPTDVQAEAT-RKAARMVWVANLLVFCVCPFLPHVGLTVRLAYGWNAC 248  
Db 223 CSSVVLRTL--RKATLSQIGTNKKVLMITVHMAVFCVFPVNSVLFVALVRSQAI 280  
  
QY 249 --ALLETIRRALY-ITSKLSANDCCLDACIYYMAKEQOEASALAVAPRAKAKHSQDSLC 305  
Db 281 TNCFLERFAKIMYPITLCLATLNCDFPFIYFTLESFQKSFYI-----NAHIRMESLIF 334  
  
QY 306 VT 307  
Db 335 KT 336

RESULT 12

US-10-617-217A-176  
; Sequence 176, Application US/10617217A  
; Publication No. US20040081986A1  
; GENERAL INFORMATION:  
; APPLICANT: MATSUDA, Akio et al.  
; TITLE OF INVENTION: NF-kB ACTIVATING GENE  
; FILE REFERENCE: 1254-0229P  
; CURRENT APPLICATION NUMBER: US/10/617,217A  
; PRIOR FILING DATE: 2003-07-11  
; PRIOR APPLICATION NUMBER: JP 2000-402288  
; PRIOR FILING DATE: 2000-12-28  
; PRIOR APPLICATION NUMBER: JP 2001-088912  
; PRIOR FILING DATE: 2001-03-26  
; PRIOR APPLICATION NUMBER: JP 2001-254018  
; PRIOR FILING DATE: 2001-08-24  
; PRIOR APPLICATION NUMBER: US 60/258,315  
; PRIOR FILING DATE: 2000-12-28  
; PRIOR APPLICATION NUMBER: US 60/278,640  
; PRIOR FILING DATE: 2001-03-26  
; PRIOR APPLICATION NUMBER: US 60/314,385  
; PRIOR FILING DATE: 2001-08-24  
; NUMBER OF SEQ ID NOS: 224

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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 176
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-617-217A-176

Query Match      24.9%; Score 402; DB 4; Length 370;
Best Local Similarity 34.1%; Pred. No. 8.2e-30;
Matches 103; Conservative 60; Mismatches 111; Indels 28; Gaps 10;

QY 25 AYGLVLLVGLLLNSLALWVFCRMOQWETRIYMTNLAVADCLCTLPF-VLHSLR-- 81
Db 44 AVSVVFIILGILITNSVSLVFCFRMKRSETAIFITNLAVSDLLFVCTLPFKIFYNFRH 103
QY 82 -DTSPTPLCQLSQGIYLTNRNYSISLVTAIVDRYVAVRHPLRARGLSRQAAACAVL 140
Db 104 WPFQDT-LCKISGTAFITNIYGMFLFTICISVDRFLAIVYPPFRSRTIRTRNSAIVCAGV 162
QY 141 WLVIGSLVARWLLGQEQ-----GGFCFRSTRHNFSMR--PPLLGFYPLAVVVF 189
Db 163 WILVLSGGISASLFTSTNNVNNATTCFEGFSKRWKTYLSKITIFIEVVGFIPLILNVS 222
QY 190 CSLKVVTTALAQRPPTDVGQAEAT-RKAARMVMANLLVFWVCFPLHLVGLTVRLAVGWNAC 248
Db 223 CSSVVLRTL--RKPATLSQIGTKKKVLMKMTVHMAVFWVCFVYNSVLFYALVRSQAI 280
QY 249 --ALLETIRRALY-ITSKLSANDCCCLDAICYYYMAKEFOEASALAVAPRAKAHKSQDSL 305
Db 281 TNCFLERPAKIMYPITCLATLNCDDPFIYYFTLESFQKSFYI-----NAHIRMESLF 334
QY 306 VT 307
Db 335 KT 336

RESULT 14
US-10-024-298A-176
; Sequence 176, Application US/10024298A
; Publication No. US20040214167A9
; GENERAL INFORMATION:
; APPLICANT: ASAH KASEI KABUSHIKI KAISHA
; APPLICANT: AKIO MATSUDA
; APPLICANT: GOICHI HONDA
; APPLICANT: SHUJI MURAMATSU
; APPLICANT: YUKIKO NAGANO
; TITLE OF INVENTION: NP-K B Activating Gene
; FILE REFERENCE: 1254-0191P
; CURRENT APPLICATION NUMBER: US/10/024,298A
; CURRENT FILING DATE: 2003-04-08
; PRIOR APPLICATION NUMBER: 60/314,385
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 60/278,641
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: 60/258,315
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: JP254018/2001
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: JP0088912/2001
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: JP402288/2000
; PRIOR FILING DATE: 2000-12-28
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 176
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-024-298A-176

Query Match      24.9%; Score 402; DB 4; Length 370;
Best Local Similarity 34.1%; Pred. No. 8.2e-30;
Matches 103; Conservative 60; Mismatches 111; Indels 28; Gaps 10;

QY 25 AYGLVLLVGLLLNSLALWVFCRMOQWETRIYMTNLAVADCLCTLPF-VLHSLR-- 81
Db 44 AVSVVFIILGILITNSVSLVFCFRMKRSETAIFITNLAVSDLLFVCTLPFKIFYNFRH 103
QY 82 -DTSPTPLCQLSQGIYLTNRNYSISLVTAIVDRYVAVRHPLRARGLSRQAAACAVL 140
Db 104 WPFQDT-LCKISGTAFITNIYGMFLFTICISVDRFLAIVYPPFRSRTIRTRNSAIVCAGV 162
QY 141 WLVIGSLVARWLLGQEQ-----GGFCFRSTRHNFSMR--PPLLGFYPLAVVVF 189
Db 163 WILVLSGGISASLFTSTNNVNNATTCFEGFSKRWKTYLSKITIFIEVVGFIPLILNVS 222
QY 190 CSLKVVTTALAQRPPTDVGQAEAT-RKAARMVMANLLVFWVCFPLHLVGLTVRLAVGWNAC 248
Db 223 CSSVVLRTL--RKPATLSQIGTKKKVLMKMTVHMAVFWVCFVYNSVLFYALVRSQAI 280
QY 249 --ALLETIRRALY-ITSKLSANDCCCLDAICYYYMAKEFOEASALAVAPRAKAHKSQDSL 305
Db 281 TNCFLERPAKIMYPITCLATLNCDDPFIYYFTLESFQKSFYI-----NAHIRMESLF 334
QY 306 VT 307
Db 335 KT 336

RESULT 13
US-10-775-965-11
; Sequence 11, Application US/10775965
; Publication No. US20040209808A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; APPLICANT: Kornacker, Michael
; TITLE OF INVENTION: MODULATORS OF HUMAN G-PROTEIN COUPLED RECEPTORS
; FILE REFERENCE: D0286 NP
; CURRENT APPLICATION NUMBER: US/10/775,965
; CURRENT FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: U.S. 60/446,655
; PRIOR FILING DATE: 2003-02-11
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 11
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-775-965-11

Query Match      24.9%; Score 402; DB 4; Length 370;
Best Local Similarity 34.1%; Pred. No. 8.2e-30;
Matches 103; Conservative 60; Mismatches 111; Indels 28; Gaps 10;

QY 25 AYGLVLLVGLLLNSLALWVFCRMOQWETRIYMTNLAVADCLCTLPF-VLHSLR-- 81
Db 44 AVSVVFIILGILITNSVSLVFCFRMKRSETAIFITNLAVSDLLFVCTLPFKIFYNFRH 103
QY 82 -DTSPTPLCQLSQGIYLTNRNYSISLVTAIVDRYVAVRHPLRARGLSRQAAACAVL 140
Db 104 WPFQDT-LCKISGTAFITNIYGMFLFTICISVDRFLAIVYPPFRSRTIRTRNSAIVCAGV 162
QY 141 WLVIGSLVARWLLGQEQ-----GGFCFRSTRHNFSMR--PPLLGFYPLAVVVF 189
Db 163 WILVLSGGISASLFTSTNNVNNATTCFEGFSKRWKTYLSKITIFIEVVGFIPLILNVS 222
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Qy 190 CSLKVVTTALQRPPTDVQAEAT-RKAARMVWNLIVFVVCFLPLHVGLTVRLAVGNAC 248  
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Qy 249 --ALLETTIRALY-ITSKLSDANCCLDIAICVYVMKEFOEASALAVAPRAKAKHSQDSLC 305  
Db 281 TNCFLERFAKIMYPITICLATLNCDDFFIYFTLESFQKSFYI-----NAHIRMESLP 334  
Qy 306 VT 307  
Db 335 KT 336

Search completed: February 9, 2006, 01:21:15  
Job time : 120.5 secs

Db 335 KT 336  
US-10-753-267-86  
; Sequence 86, Application US/10753267  
; Publication No. US20050037946A1  
; GENERAL INFORMATION:  
; APPLICANT: Millennium Pharmaceuticals, Inc.  
; APPLICANT: Stegiano, Nancy E.  
; APPLICANT: Healy, Aileen  
; APPLICANT: Acton, Susan L.  
; APPLICANT: Galvin, Katherine M.  
; APPLICANT: Donoghue, Mary A.  
; APPLICANT: Rodriguez-Way, Amelie  
; APPLICANT: Tomlinson, James E.  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING  
; TITLE OF INVENTION: CARDIOVASCULAR DISEASE USING 1722, 10280, 59917, 85553,  
; TITLE OF INVENTION: 10653, 9235, 21668, 17794, 2210, 6169, 10102, 21061, 17662,  
; TITLE OF INVENTION: 1468, 12282, 6350, 9035, 1820, 23652, 7301, 8925, 8701,  
; TITLE OF INVENTION: 3533, 9462, 9123, 12788, 17729, 65552, 1261, 21476, 33770,  
; TITLE OF INVENTION: 9380, 2569654, 33556, 44143, 32612, 10671, 261,  
; TITLE OF INVENTION: 44570, 41922, 2552, 2417, 19319, 43969, 8921, 8993, 955,  
; TITLE OF INVENTION: 32345, 966, 1920, 17318, 1510, 14180, 26005, 554, 16408,  
; TITLE OF INVENTION: 42028, 112091, 13886, 13942, 1673, 54946 OR 2419  
; FILE REFERENCE: MP103-003P1RNMIM  
; CURRENT APPLICATION NUMBER: US/10/753,267  
; CURRENT FILING DATE: 2004-01-08  
; PRIOR APPLICATION NUMBER: US 60/439,683  
; PRIOR FILING DATE: 2003-01-13  
; PRIOR APPLICATION NUMBER: US 60/445,216  
; PRIOR FILING DATE: 2003-02-05  
; PRIOR APPLICATION NUMBER: US 60/448,036  
; PRIOR FILING DATE: 2003-02-18  
; PRIOR APPLICATION NUMBER: US 60/454,189  
; PRIOR FILING DATE: 2003-03-12  
; PRIOR APPLICATION NUMBER: US 60/457,541  
; PRIOR FILING DATE: 2003-03-25  
; PRIOR APPLICATION NUMBER: US 60/466,411  
; PRIOR FILING DATE: 2003-04-29  
; PRIOR APPLICATION NUMBER: US 60/469,041  
; PRIOR FILING DATE: 2003-05-08  
; PRIOR APPLICATION NUMBER: US 60/477,414  
; PRIOR FILING DATE: 2003-06-10  
; PRIOR APPLICATION NUMBER: US 60/478,560  
; PRIOR FILING DATE: 2003-06-13  
; PRIOR APPLICATION NUMBER: US 60/489,772  
; PRIOR FILING DATE: 2003-07-24  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 130  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 86  
; LENGTH: 370  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-10-753-267-86

Query Match 24.9%; Score 402; DB 5; Length 370;  
Best Local Similarity 34.1%; Pred. No. 8.2e-30;  
Matches 103; Conservative 60; Mismatches 111; Indels 28; Gaps 10;  
Qy 25 AYGLVLLVGLLINSIALWFCRMOQWETRIYMTNLAVADICLLCTLPF-VLHSLR-- 81  
Db 44 AVSVVVFILGLITNSVSLVFCFRMKRSETAIFITNLAVSDLLFVCTLPFPKIFYNFRH 103  
Qy 82 -DTSPTPLCOLSQGIYLTNRYSISLVAIAVDYVAVRHPLRARGLRSPROAAVCAVL 140  
Db 104 WPFQGT-LCKISTAFLTNIYGSMLFLTICISVDRLAIVPFRSRTIRRRNSAIVCAGV 162  
Qy 141 WVLVIGSLVARMILGIGQE-----GGFCFRSTRHNFNSMR--PPLLGfYLP LAVVVF 189  
Db 163 WILVLSGGISASLFSFTTNNVNTTTCFEGFSKRVKWTLSKITFIETVVVGFIPLNLVS 222

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GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: February 9, 2006, 01:17:29 ; Search time 10.5 Seconds  
(without alignments)  
386.178 Million cell updates/sec

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Sequence: 1 MNGTYNTCGSSDLTPPAIK.....AVAPRAKHSQDSLCVTLA 309

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 97014 seqs, 1312538 residues

Total number of hits satisfying chosen parameters: 97014

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA New:  
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4: /cgm2\_6/ptodata/1/pubpaa/PCT NEW PUB.pap.\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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|------------|-------|---------------|--------|----|----------------------|
| 1          | 334.5 | 20.7          | 254    | 6  | US-10-055-877-248    |
| 2          | 334.5 | 20.7          | 254    | 6  | US-10-055-877-327    |
| 3          | 334.5 | 20.7          | 254    | 6  | US-10-055-877-340    |
| 4          | 334.5 | 20.7          | 254    | 6  | US-10-055-877-346-83 |
| 5          | 317.5 | 19.7          | 346    | 7  | US-11-157-930-2      |
| 6          | 315.5 | 19.5          | 365    | 6  | US-10-055-877-545    |
| 7          | 312.5 | 18.4          | 391    | 7  | US-11-127-877-52     |
| 8          | 305   | 18.9          | 259    | 6  | US-10-055-877-225    |
| 9          | 305   | 18.9          | 259    | 6  | US-10-055-877-237    |
| 10         | 300   | 18.6          | 339    | 7  | US-11-157-930-4      |
| 11         | 300   | 18.6          | 367    | 7  | US-11-157-930-6      |
| 12         | 298.5 | 18.5          | 373    | 7  | US-11-127-877-46     |
| 13         | 297.5 | 18.4          | 358    | 7  | US-11-127-877-66     |
| 14         | 288.5 | 17.9          | 352    | 6  | US-10-055-877-523    |
| 15         | 288.5 | 17.9          | 352    | 7  | US-11-068-686-2      |
| 16         | 288.5 | 17.9          | 352    | 7  | US-11-127-877-61     |
| 17         | 287.5 | 17.8          | 352    | 7  | US-11-068-686-20     |
| 18         | 275.5 | 17.1          | 337    | 7  | US-11-157-930-5      |
| 19         | 270.5 | 16.8          | 375    | 7  | US-11-127-877-67     |
| 20         | 263.5 | 16.3          | 374    | 7  | US-11-127-877-62     |
| 21         | 255.5 | 15.8          | 359    | 6  | US-10-055-877-712    |
| 22         | 255.5 | 15.8          | 359    | 6  | US-10-055-877-716    |
| 23         | 255.5 | 15.8          | 359    | 6  | US-10-876-787-2      |
| 24         | 255.5 | 15.8          | 359    | 7  | US-11-127-877-65     |
| 25         | 255.5 | 15.8          | 388    | 6  | US-10-055-877-713    |

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Sequence 715, App  
Sequence 55, Appl  
Sequence 934, App  
Sequence 2, Appli  
Sequence 838, App  
Sequence 837, App  
Sequence 161, App  
Sequence 60, Appli  
Sequence 4, Appli  
Sequence 64, Appli  
Sequence 36, Appli  
Sequence 636, App  
Sequence 637, App  
Sequence 12, Appl  
Sequence 24, Appl  
Sequence 6, Appli  
Sequence 59, Appl  
Sequence 32, Appl

ALIGNMENTS

RESULT 1  
US-10-055-877-248  
; Sequence 248 Application US/10055877  
; Publication No. US2005028241A1  
; GENERAL INFORMATION:  
; APPLICANT: DeCristofaro, Marc  
; APPLICANT: Padigaru, Muralidhara  
; APPLICANT: Miller, Charles  
; APPLICANT: Tchernev, Velizar  
; APPLICANT: Zhong, Mei  
; APPLICANT: Anderson, David  
; APPLICANT: Ballinger, Robert  
; APPLICANT: Gerlach, Valerie  
; APPLICANT: Spytek, Kimberly  
; APPLICANT: Ratelli, Luca  
; APPLICANT: Kekuda, Ramesh  
; APPLICANT: Guo, Xiaojia  
; APPLICANT: Zerhusen, Bryan  
; APPLICANT: Andrew, David  
; APPLICANT: Mezes, Peter  
; APPLICANT: Patturajan, Meera  
; APPLICANT: Burgess, Catherine  
; APPLICANT: Eisen, Andrew  
; APPLICANT: Wolenc, Adam  
; APPLICANT: Baumgartner, Jason  
; APPLICANT: Shinkets, Richard  
; APPLICANT: Gusev, Vladimir  
; APPLICANT: Vernet, Corine  
; APPLICANT: Taupier Jr., Raymond  
; APPLICANT: Pena, Carol  
; APPLICANT: Shenoy, Suresh  
; APPLICANT: Li, Li  
; APPLICANT: Casman, Stacie  
; APPLICANT: Boldog, Ference  
; TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoded Thereby  
; FILE REFERENCE: 21402-251  
; CURRENT APPLICATION NUMBER: US/10/055,877  
; CURRENT FILING DATE: 2002-01-22  
; PRIOR APPLICATION NUMBER: 60/262,892  
; PRIOR FILING DATE: 2001-01-19  
; PRIOR APPLICATION NUMBER: 60/263,598  
; PRIOR FILING DATE: 2001-01-23  
; PRIOR APPLICATION NUMBER: 60/263,799  
; PRIOR FILING DATE: 2001-01-24  
; PRIOR APPLICATION NUMBER: 60/264,117  
; PRIOR FILING DATE: 2001-01-25  
; PRIOR APPLICATION NUMBER: 60/264,139  
; PRIOR FILING DATE: 2001-01-25

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; PRIOR APPLICATION NUMBER: 60/264,478
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/263,351
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/272,870
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 60/275,990
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/275,927
; PRIOR FILING DATE: 2001-03-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 512
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 248
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Description of Artificial Sequence: 7tm_1, 7
; OTHER INFORMATION: transmembrane receptor domain
US-10-055-877-248

Query Match      20.7%; Score 334.5; DB 6; Length 254;
Best Local Similarity 34.1%; Pred. No. 2.2e-25;
Matches 92; Conservative 54; Mismatches 87; Indels 37; Gaps 9;

QY 28 GVLLVGLLLNSLALWVFCRMOQMTETRIYMTNLAVADLCLCTL-PFVLHSLRD---T 83
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QY 84 SDTPLCQLSQGIYLTNRYSISLVTAIVDRYVAVRHPLRARGLSRPRQAAAVCAVLWL 143
Db 52 FGDAKCKLVGALFVNGYASILLTALSIDRYLAIVHPLRYRIRTPRAKVLILLVWL 111

QY 144 V-----IGSLVARMLLGIQEGG-----FCFRSTRHNFNSMRPPLLGFLYPLAVVVFCSL 192
Db 112 ALLSLPPLFLSWLRTVEGNTTVCLIDPPESSVKRSY-VLLSTLVGFVPLVILVCYT 170

QY 193 KVVTAQAQRPPTDVG---QAEATRKAAARMVWNLVVFVCFPLHVLTVRLAVGNAC 249
Db 171 RILRTLKRARSQSRSLKRSSSRKAOKMLLVVVVFLVCWLPYHIVLL-----DSL 224

QY 250 LLETIR---RALYITSKLSDANCLDAICY 276
Db 225 LLSIWRVLPALLITLWLVNLSCLNPIY 254

RESULT 2
US-10-055-877-327
; Sequence 327, Application US/10055877
; Publication No. US20050288241A1
; GENERAL INFORMATION:
; APPLICANT: DeCristofaro, Marc
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Miller, Charles
; APPLICANT: Tchernev, Velizar
; APPLICANT: Zhong, Mei
; APPLICANT: Anderson, David
; APPLICANT: Ballinger, Robert
; APPLICANT: Gerlach, Valerie
; APPLICANT: Spytak, Kimberly
; APPLICANT: Ratelli, Luca
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Guo, Xiaojia
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Andrew, David
; APPLICANT: Mezes, Peter
; APPLICANT: Patturajan, Meera
; APPLICANT: Burgess, Cahterine
; APPLICANT: Eisen, Andrew
; APPLICANT: Wolenc, Adam
; APPLICANT: Baumgartner, Jason
; APPLICANT: Shimkets, Richard

```

```

; APPLICANT: Gusev, Vladimir
; APPLICANT: Vernet, Corine
; APPLICANT: Taupier Jr., Raymond
; APPLICANT: Pena, Carol
; APPLICANT: Shenoy, Suresh
; APPLICANT: Li, Li
; APPLICANT: Casman, Stacie
; APPLICANT: Boldog, Ference
; TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoded Thereby
; FILE REFERENCE: 21402-251
; CURRENT APPLICATION NUMBER: US/10/055,877
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: 60/262,892
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: 60/263,598
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 60/263,799
; PRIOR FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: 60/264,117
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/264,139
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/264,478
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/263,351
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/272,870
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 60/275,990
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/275,927
; PRIOR FILING DATE: 2001-03-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 512
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 327
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: 7tm_1, 7
; OTHER INFORMATION: transmembrane receptor domain consensus sequence
US-10-055-877-327

Query Match      20.7%; Score 334.5; DB 6; Length 254;
Best Local Similarity 34.1%; Pred. No. 2.2e-25;
Matches 92; Conservative 54; Mismatches 87; Indels 37; Gaps 9;

QY 28 GVLLVGLLLNSLALWVFCRMOQMTETRIYMTNLAVADLCLCTL-PFVLHSLRD---T 83
Db 1 GNLLVILVILRTKCL-----RTPTNIFLNLAVADLFLLLTPPWALYLVGGDWV 51

QY 84 SDTPLCQLSQGIYLTNRYSISLVTAIVDRYVAVRHPLRARGLSRPRQAAAVCAVLWL 143
Db 52 FGDAKCKLVGALFVNGYASILLTALSIDRYLAIVHPLRYRIRTPRAKVLILLVWL 111

QY 144 V-----IGSLVARMLLGIQEGG-----FCFRSTRHNFNSMRPPLLGFLYPLAVVVFCSL 192
Db 112 ALLSLPPLFLSWLRTVEGNTTVCLIDPPESSVKRSY-VLLSTLVGFVPLVILVCYT 170

QY 193 KVVTAQAQRPPTDVG---QAEATRKAAARMVWNLVVFVCFPLHVLTVRLAVGNAC 249
Db 171 RILRTLKRARSQSRSLKRSSSRKAOKMLLVVVVFLVCWLPYHIVLL-----DSL 224

QY 250 LLETIR---RALYITSKLSDANCLDAICY 276
Db 225 LLSIWRVLPALLITLWLVNLSCLNPIY 254

RESULT 3
US-10-055-877-340
; Sequence 340, Application US/10055877
; Publication No. US20050288241A1

```



US-10-877-346-83

Query Match 20.7%; Score 334.5; DB 6; Length 254;  
Best Local Similarity 34.1%; Pred. No. 2.2e-25;  
Matches 92; Conservative 54; Mismatches 87; Indels 37; Gaps 9;

Qy 28 GVLLVGLLNSLWVFCRCMQMTETRIYMTNLAVADICLCTL-PFVHSLRD---T 83  
Db 1 GNLLVILVILTKKL-----RPTNIFLNLAVADLFLTPPWALYVLVGGDWV 51

Qy 84 SDTFLQQLSQGIYLTNRYMSISLVTAIVDRYVAVRHPLRARGLRSPROAAVCAVLWVL 143  
Db 52 FGDALCKVGLFVNGYASILLTAISIDYLAIVHPLRYRIRTPRAKVLILLVWL 111

Qy 144 V-----TGLVARMLLGIQEGG-----FCFRSTRNFMSPRLPLGLFYPLAVVVFCSL 192  
Db 112 ALLSLPPLLFSWLRTVEGNTTVCLIDFPESVGRSY-VLLSTLVGVFLPLVILVCYT 170

Qy 193 KVTALAQRPPTDVG---QAEATKAAKRWYMANLLVVFVCFPLHVGLTVRLAVGNACA 249  
Db 171 RLRLTLKRAQSRLKRRSSSRKAAMLLVVVVVFLVCWLPYHIVLLL-----DSL 224

Qy 250 LLETIR---RALYITSKLSANCLDAICY 276  
Db 225 LLSIWRVLPALITLWLVNCLNPIY 254

RESULT 5

US-11-157-930-2  
; Sequence 2, Application US/11157930  
; Publication No. US20050266482A1  
; GENERAL INFORMATION:  
; APPLICANT: Xiao, Yonghong  
; TITLE OF INVENTION: Regulation of Human CysLT2-Like GPCR  
; FILE REFERENCE: 04974.00458  
; CURRENT APPLICATION NUMBER: US/11/157,930  
; PRIOR FILING DATE: 2005-06-22  
; PRIOR APPLICATION NUMBER: US/09/828,478  
; PRIOR FILING DATE: 2001-04-09  
; PRIOR FILING DATE: 2000-04-07  
; PRIOR APPLICATION NUMBER: 60/254,876  
; PRIOR FILING DATE: 2000-12-13  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 346  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-157-930-2

Query Match 19.7%; Score 317.5; DB 7; Length 346;  
Best Local Similarity 28.4%; Pred. No. 1.4e-23;  
Matches 89; Conservative 64; Mismatches 139; Indels 21; Gaps 10;

Qy 2 NGTYTCSSDLTPWPAIKLGFY--AYLGVLLVGLLNSLWVFCRCMQMTETRIYM 59  
Db 20 NGTFNNNSRNCI-IENFKREFPIVYL-IFFGVGLNGLSIVVFLQPYKKSTSVNFM 77

Qy 60 TNLAVADICLCTLPP-VLHSLRDTs-----DTPLCQLSQGIYLTNRYMSISLVTAIVDR 114  
Db 78 LNLAISDLLPSTLPPFRADYLRGNSWIFGDLACRIMSLSLYV-NMYSIYFLTVLSVR 136

Qy 115 YVAVRHPLRARGLRSPROAAVCAVLWVLVIGSVIARMLLGIQEGG---FCFRSTRNFM 171  
Db 137 FLAWHPEFRLLHVTISIRANILCOIILWILMSIMLLDSGSGNGSVTSCLEINLYKIA 196

Qy 172 SMRPP-----LLGPLYLAVVVFCSLKVVTALAQRPPTDVGOAETKAAKRWYMANLLVF 226  
Db 197 KLQTMNYIALVVGCLLPFTLSICLLIIRVLLKVEVPESGLRVSHRKALTTIITLIIF 256

Qy 227 VVCFPLHVGLTVRLAVGNACALLETIRALYITSKLSANCLDAICYMKEPQE- 285

Db 257 FLCFLPYHTLRVHLTT-WKVGCLKDRHLKALVITLALAAANACFNPLLYFAGENFKDR 315  
Qy 286 -ASALAVAPRAKA 297  
Db 316 LKSALRKGHPOKA 328

RESULT 6

US-10-995-561-545  
; Sequence 545, Application US/10995561  
; Publication No. US20050272054A1  
; GENERAL INFORMATION:  
; APPLICANT: CARGILL, Michele et al.  
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF  
; FILE REFERENCE: CL001559  
; CURRENT APPLICATION NUMBER: US/10/995,561  
; CURRENT FILING DATE: 2004-11-24  
; NUMBER OF SEQ ID NOS: 85702  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 545  
; LENGTH: 365  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-995-561-545

Query Match 19.5%; Score 315.5; DB 6; Length 365;  
Best Local Similarity 29.1%; Pred. No. 2.3e-23;  
Matches 93; Conservative 55; Mismatches 127; Indels 45; Gaps 11;

Qy 29 VLLVGLLNSLWVFCRCMQMTETRIYMTNLAVADICLCTLPLFVHSLRDTSDTP- 87  
Db 44 VVFLVGLGLNAPTLMFLFRLRPWDATATYMFHLASDTLYVLSLPTLIYYAAHNHMPF 103

Qy 88 ---LQQLSQGIYLTNRYMSISLVTAIVDRYVAVRHPLRARGLRSPROAAVCAVLWVL 144  
Db 104 GTEICKPVRPLFMYNLYCSVLFLTCISVHYRIGIICPLRALWGRPLAGLCLAVLWLV 163

Qy 145 IGSVLAR-WLLGIQEGG---FCFRSTR-----H--NFNSMRFPFLGFLYPLAVVVFCSLK 193  
Db 164 AGCLVPLNFFVTSNKGTIVLCHDITRPEFDHYVHFSSAVMGLL-FGVPCLVTLVCYGL 222

Qy 194 VVTLAQRPPTDVGOAETKAAKRWYMANLLVVFVCFPLHVGLTV-----RLAVGNACA 249  
Db 223 MARRLYQ-PLPGSAQSSSRSLRSLRTIAVVLTVFAVCFVPHITRTIYYLARLEA--DCR 279

Qy 250 LLETIRALYITSKLSANCLDAICYMKEPQE-----ASALAVAP 293  
Db 280 VLNIVNVVYKVRPLASANSCLDPVLLYLTGDKYRRLQRLCGGKGPQPRTAASLALVS 339

Qy 294 RAK-----AHKSQDSLCTV 307  
Db 340 LPEDSSCRWAATPQDSSCST 359

RESULT 7

US-11-127-877-52  
; Sequence 52, Application US/11127877  
; Publication No. US20050287565A1  
; GENERAL INFORMATION:  
; APPLICANT: Merckhiers, Pascal G.  
; APPLICANT: Hoffmann, Marcel  
; APPLICANT: Spittael, Koenraad F. F.  
; APPLICANT: Laenen, Wendy  
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting  
; TITLE OF INVENTION: Amyloid-Beta Protein Production  
; FILE REFERENCE: P27,800-B USA  
; CURRENT APPLICATION NUMBER: US/11/127,877  
; CURRENT FILING DATE: 2005-05-12  
; PRIOR APPLICATION NUMBER: 60/570,352  
; PRIOR FILING DATE: 2004-05-12



```

; TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoded Thereby
; FILE REFERENCE: 21402-251
; CURRENT APPLICATION NUMBER: US/10/055,877
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: 60/262,892
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: 60/263,598
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 60/263,799
; PRIOR FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: 60/264,117
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/264,139
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/264,478
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/263,351
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/272,870
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 60/275,990
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/275,927
; PRIOR FILING DATE: 2001-03-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 512
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 225
; LENGTH: 259
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: 7tm_1 domain
; OTHER INFORMATION: consensus sequence
US-10-055-877-225

Query Match      18.9%; Score 305; DB 6; Length 259;
Best Local Similarity 33.0%; Pred. No. 1.6e-22;
Matches 93; Conservative 49; Mismatches 84; Indels 56; Gaps 10;

QY 28 GVLLVLGLLNSLALWVFCRMOQWTETRIYMTNLAVADLCLLCTL-PFVLHSLRDTSD- 85
DB 1 GNLLVLVLRTKGL-----RTPTNIFILNLAVADLLFLTLPPWALYVLVGSGS 51
QY 86 ----TPLCQSQGIYLTNRYMSISLVTAIVDRYVAVVPHPLRAGLR-SPROAAVCAVL 140
DB 52 WPFGSALCKLVATLDVWVWYASILLTATISIDRYLAIVPHLYRRRTSPRRKVVILLV 111
QY 141 WVLV----IGSLVARWLLGIQEGG-----FCFSTRHNFNSMR-----PPLL 178
DB 112 WVLALLSLPPLLFSWVKTVBEGNGTLNANNVTCLIDPFESTASVWTLKSYLLSTLV 171
QY 179 GFVLPLAVVFCSLKVVTTALAQRPPTDVQAEATKAAKRMVWVWVNLVFCPLPLHVLG- 237
DB 172 GFLLPLVLIVCVTRILRTL-----RKAATLLVVVVVFLVCLWLPYFIVLL 217
QY 238 --TVRLAVGWNA-CALLETIRALYITSKLSDANCLDAICY 276
DB 218 LDTCLSIIMSSTCELERVLPALTALLVTLWLVAYVNSCLNPIIY 259

RESULT 9
US-10-055-877-237
; Sequence 237, Application US/10055877
; Publication No. US20050288241A1
; GENERAL INFORMATION:
; APPLICANT: Decristofaro, Marc
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Miller, Charles
; APPLICANT: Tchernev, Velizar
; APPLICANT: Zhong, Mei
; APPLICANT: Anderson, David
; APPLICANT: Ballinger, Robert

; PRIOR APPLICATION NUMBER: 60/603,948
; PRIOR FILING DATE: 2004-08-24
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 52
; LENGTH: 391
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-127-877-52

Query Match      19.4%; Score 312.5; DB 7; Length 391;
Best Local Similarity 27.6%; Pred. No. 4.9e-23;
Matches 89; Conservative 54; Mismatches 128; Indels 51; Gaps 9;

QY 1 MNGTYNTCGSSDLTW-----PPAIKLGFEYAYILGVLLVLGLLNSLALWVFCRMOQW 52
DB 38 LNGTHPAQSCPQVEWLGMLNTIQQP-----FLWLVFLVATLENIFVLSVFLKHSK 89
QY 53 TETRIYMTNLAVADLCLLCTLPFVLHSLRDTSD-----TPLCQSQGIYLTNRYMSISLV 108
DB 90 TVAEIYLGNAADLILACGLFPFAITISNPNDFMLFGETLCRVVNAIISMNLYSSICFLM 149
QY 109 ATADVRYVAVRPHLRARGERSPROAAVCAVLW--VLVIGS--LVARWLLGIQEGGCFR 164
DB 150 LVSIDRYLALVKTMSGMRGVRWAKLVSLVITWGTLLSSPMLVFRITMKEYSDEG---- 205
QY 165 STRHN-----FNSMRPFLGFLYPLAVVFCSLKVVTTALAQRPPTDVGOA 209
DB 206 ---HNVACVISVPSLIVEFTNMLNVGVLLPLSVITFCTMQIMQVLRNEMQKFEI 262
QY 210 EATRKAAARMVWVNLVVFVFCPLHVLGTV-----RLAVGWNA-CALLETIRALYITSKLS 265
DB 263 QTERRATVNLVLLVLLFIICWLPFOISTPLDTLHLRGI-LSSQCDERIIDVITQISFMA 321
QY 266 DANCCLDAICYWMAKEFOEAS 287
DB 322 YNSCLNPLVYIVGKRFKKK 343

RESULT 8
US-10-055-877-225
; Sequence 225, Application US/10055877
; Publication No. US20050288241A1
; GENERAL INFORMATION:
; APPLICANT: Decristofaro, Marc
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Miller, Charles
; APPLICANT: Tchernev, Velizar
; APPLICANT: Zhong, Mei
; APPLICANT: Anderson, David
; APPLICANT: Ballinger, Robert
; APPLICANT: Gerlach, Valerie
; APPLICANT: Spytek, Kimberly
; APPLICANT: Ratelli, Luca
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Guo, Xiaojia
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Andrew, David
; APPLICANT: Mezes, Peter
; APPLICANT: Patturajan, Meera
; APPLICANT: Burgess, Cahterine
; APPLICANT: Eisen, Andrew
; APPLICANT: Wolenc, Adam
; APPLICANT: Baumgartner, Jason
; APPLICANT: Shimkets, Richard
; APPLICANT: Gueev, Vladimir
; APPLICANT: Vernet, Corine
; APPLICANT: Taupier Jr., Raymond
; APPLICANT: Pena, Carol
; APPLICANT: Shenoy, Suresh
; APPLICANT: Li, Li
; APPLICANT: Casman, Stacie
; APPLICANT: Boldog, Ference

```

```

: APPLICANT: Gerlach, Valerie
: APPLICANT: Spytek, Kimberly
: APPLICANT: Ratelli, Luca
: APPLICANT: Kekuda, Ramesh
: APPLICANT: Guo, Xiaojia
: APPLICANT: Zarhusen, Bryan
: APPLICANT: Andrew, David
: APPLICANT: Mezes, Peter
: APPLICANT: Patturajan, Meera
: APPLICANT: Burgess, Catherine
: APPLICANT: Elsen, Andrew
: APPLICANT: Wolenc, Adam
: APPLICANT: Baumgartner, Jason
: APPLICANT: Shimkets, Richard
: APPLICANT: Gusev, Vladimir
: APPLICANT: Vernet, Corine
: APPLICANT: Taupier Jr., Raymond
: APPLICANT: Pena, Carol
: APPLICANT: Shenoy, Suresh
: APPLICANT: Li, Li
: APPLICANT: Casman, Stacie
: APPLICANT: Boldog, Ference
: TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoded Thereby
: FILE REFERENCE: 21402-251
: CURRENT APPLICATION NUMBER: US/10/055,877
: CURRENT FILING DATE: 2002-01-22
: PRIOR APPLICATION NUMBER: 60/262,892
: PRIOR FILING DATE: 2001-01-19
: PRIOR APPLICATION NUMBER: 60/263,598
: PRIOR FILING DATE: 2001-01-23
: PRIOR APPLICATION NUMBER: 60/263,799
: PRIOR FILING DATE: 2001-01-24
: PRIOR APPLICATION NUMBER: 60/264,117
: PRIOR FILING DATE: 2001-01-25
: PRIOR APPLICATION NUMBER: 60/264,139
: PRIOR FILING DATE: 2001-01-25
: PRIOR APPLICATION NUMBER: 60/264,478
: PRIOR FILING DATE: 2001-01-26
: PRIOR APPLICATION NUMBER: 60/263,351
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: 60/272,870
: PRIOR FILING DATE: 2001-03-02
: PRIOR APPLICATION NUMBER: 60/275,990
: PRIOR FILING DATE: 2001-03-14
: PRIOR APPLICATION NUMBER: 60/275,927
: PRIOR FILING DATE: 2001-03-14
: REMAINING Prior Application data removed - See File Wrapper or PALM.
: NUMBER OF SEQ ID NOS: 512
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 237
: LENGTH: 259
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: 7cm_1 domain
: OTHER INFORMATION: consensus sequence
: US-10-055-877-237

```

|    |     |   |     |
|----|-----|---|-----|
| QY | 179 | GFYPPLAVVFCSLKVVTAQAORPTDVGQAEATKAARMWVANLLVFVVCFLPHVLGL-                 | 237 |
|    |     | :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   : |     |
| Db | 172 | GFLPPLLVLVCYTIRLSTL-----RKAARTLLVVVVVFLCWLCPYFILL                         | 217 |
| QY | 238 | --TVRLAVGNNA-CALLETTRALRYITSKLSDANCLDAICY                                 | 276 |
|    |     | :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   : |     |
| Dd | 218 | LDTLCLSITMSSTCELERVLPALTLLVTIWLAYVNSCLNPIIY                               | 259 |

```

RESULT 10
US-11-157-930-4
; Sequence 4, Application US/11157930
; Publication No. US20050266482A1
; GENERAL INFORMATION:
; APPLICANT: Xieo, Yonghong
; TITLE OF INVENTION: Regulation of Human CysLT2-Like GPCR
; TITLE OF INVENTION: Protein
; FILE REFERENCE: 04974.00458
; CURRENT APPLICATION NUMBER: US/11/157,930
; CURRENT FILING DATE: 2005-06-22
; PRIOR APPLICATION NUMBER: US/09/828,478
; PRIOR FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 60/195,196
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 60/254,876
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-157-930-4

```

```

RESULT 11
US-11-157-930-6
; Sequence 6, Application US/11157930
; Publication No. US20050266482A1
; GENERAL INFORMATION:
; APPLICANT: Xiao, Yonghong
; TITLE OF INVENTION: Regulation of Human CysLT2-Like GPCR
; TITLE OF INVENTION: Protein
; FILE REFERENCE: 04974.00458

```

|    |                       |  |
|----|-----------------------|--|
|    | Query Match           | 18.5%; Score 298.5; DB 7; Length 373;                              |
|    | Best Local Similarity | 26.2%; Pred. No. 1.1e-21;  |
| Db |                       | 195 CR-----VFALTIVLEFLLPLLVTSVFTGRIMCALSR--PGLLHQGRQRVRANQLILLT 24 |



|    |     |   |     |
|----|-----|---|-----|
| Qy | 1   | MNGTYNTCGSSDLTWPPAIKLGFPYAYLGVLVLGLLNSLALWVFCCHMQQWTEIRIYMT | 60  |
| Db | 1   | MNGTYNTCGSSDLTWPPAIKLGFPYAYLGVLVLGLLNSLALWVFCCHMQQWTEIRIYMT | 60  |
| Qy | 61  | NLAVADICLLCTLPFVLHSLRDTSDTPLCOLSQIGIYLTNRWMSISLVTAIADVRAVRH | 120 |
| Db | 61  | NLAVADICLLCTLPFVLHSLRDTSDTPLCOLSQIGIYLTNRWMSISLVTAIADVRAVRH | 120 |
| Qy | 121 | PLRARGLRSPQAAAVCAVLWVLVIGSLVARWLLGIQEGGCFSTRHNFNSMRPLLGPF   | 180 |
| Db | 121 | PLRARGLRSPQAAAVCAVLWVLVIGSLVARWLLGIQEGGCFSTRHNFNSMRPLLGPF   | 180 |
| Qy | 181 | YLPNAVVFCSLKVVTALAQBPPTDVGQAETRAKAAVMWANLLVFVVCFLPHVGLTVR   | 240 |
| Db | 181 | YLPNAVVFCSLKVVTALAQBPPTDVGQAETRAKAAVMWANLLVFVVCFLPHVGLTVR   | 240 |

```

QY 241 LAVGNACALLETIRRALYITTSKLSANDCCCLDAICYYTMAKEFQASALAVAPRAKAHS 300
Db 241 LAVGNACALLETIRRALYITTSKLSANDCCCLDAICYYTMAKEFQASALAVAPRAKAHS 300

QY 301 QDSLCVTLA 309
Db 301 QDSLCVTLA 309

RESULT 2
GPR35 HUMAN
ID GPR35 HUMAN STANDARD; PRT; 309 AA.
AC QSHC97; Q43495; Q86U4;
DT 16-OCT-2001 (Rel. 40, Created)
DT 13-SEP-2005 (Rel. 48, Last sequence update)
DE 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable G-protein coupled receptor 35.
GN Name=GPR35;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE, AND VARIANT ARG-294.
RX MEDLINE=98140132; PubMed=9479505; DOI=10.1006/geno.1998.5095;
RA O'Dowd B.F., Nguyen T., Marchese A., Cheng R., Lynch K.R.,
RA Heng H.H.Q., Kolakowski L.F. Jr., George S.R.;
RT "Discovery of three novel G-protein-coupled receptor genes.";
RL Genomics 47:310-313 (1998).
RN [2]
RP NUCLEOTIDE SEQUENCE, AND VARIANTS THR-25; ILE-29; MET-108; SER-125 AND
RP MET-253.
RX MEDLINE=20472315; PubMed=11017071; DOI=10.1038/79876;
RA Horikawa Y., Oda N.J., Cox N.J., Li X., Orho-Melander M., Hara M.,
RA Hinokio Y., Lindner T.H., Mashima H., Schwarz P.E.H.,
RA del Bosque-Plata L., Horikawa Y., Oda Y., Yoshiuchi I., Colilla S.,
RA Polonsky K.S., Wei S., Concannon P., Iwasaki N., Schulze J.,
RA Baier L.J., Bogardus C., Groop L., Boerwinkle E., Hanis C.L.,
RA Ball G.I.;
RT "Genetic variation in the gene encoding calpain-10 is associated with
RT type 2 diabetes mellitus.";
RL Nat. Genet. 26:163-175 (2000).
RN [3]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RA Warren C.N., Aronstam R.S., Sharma S.V.;
RT "cDNA clones of human proteins involved in signal transduction
RT sequenced by the Guthrie cDNA resource center (www.cdna.org).";
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Orphan receptor.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -!- TISSUE SPECIFICITY: Expressed in all adult and fetal tissues
CC examined, including pancreatic islets and skeletal muscle, with
CC relatively higher levels in adult lung, small intestine, colon and
CC stomach.
CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; AF027957; AAC52028.1; -; Genomic_DNA.
CC EMBL; AF089087; AG17965.1; -; mRNA.
CC EMBL; AY275467; AAP32299.1; -; Genomic_DNA.
CC Ensembl; ENSG00000178623; Homo sapiens.
CC HGNC; HGNC:4492; GPR35.
CC MIM; 602646; -
CC GO; GO:0005887; C:integral to plasma membrane; TAS.
CC GO; GO:0004930; F:G-protein coupled receptor activity; TAS.
CC GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; TAS.
CC InterPro; IPR002076; GPCR_Rhodpsn.

DR PFAM; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCRHOOPS.
DR PROSITE; PS00237; G-PROTEIN RECEPT_F1_1; 1.
DR PROSITE; PS00262; G-PROTEIN RECEPT_F1_2; 1.
KW G-protein coupled receptor; Glycoprotein; Polymorphism; Receptor;
KW Transducer; Transmembrane.
FT TOPO_DOM 1 24 Extracellular (Potential).
FT TRANSMEM 25 45 1 (Potential).
FT TOPO_DOM 46 56 Cytoplasmic (Potential).
FT TRANSMEM 57 77 2 (Potential).
FT TOPO_DOM 78 90 Extracellular (Potential).
FT TRANSMEM 91 112 3 (Potential).
FT TOPO_DOM 113 135 Cytoplasmic (Potential).
FT TRANSMEM 136 156 4 (Potential).
FT TOPO_DOM 157 174 Extracellular (Potential).
FT TRANSMEM 175 195 5 (Potential).
FT TOPO_DOM 196 218 Cytoplasmic (Potential).
FT TRANSMEM 219 239 6 (Potential).
FT TOPO_DOM 240 258 Extracellular (Potential).
FT TRANSMEM 259 279 7 (Potential).
FT TOPO_DOM 280 309 Cytoplasmic (Potential).
FT CARBOHYD 2 2 N-linked (GlcNAc...) (Potential).
FT DISULFID 89 162 By similarity.
FT VARIANT 25 25 A -> T.
FT VARIANT 29 29 /FTID=VAR_013601.
FT VARIANT 108 108 /FTID=VAR_013602.
FT VARIANT 125 125 /FTID=VAR_013603.
FT VARIANT 253 253 /FTID=VAR_013604.
FT VARIANT 294 294 /FTID=VAR_013605.
FT CONFLICT 174 174 A -> R (in Ref. 1).
SQ SEQUENCE 309 AA; 34072 MW; 97734FB7231B26F0 CRC64;

Query Match 99.3%; Score 1602; DB 1; Length 309;
Best Local Similarity 99.4%; Pred. No. 4.9e-112;
Matches 307; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MNGTYNTCGSSDLTWPPAIKLGFYALGVILVGLIINSLALWVFCRMOQTETRIYMT 60
Db 1 MNGTYNTCGSSDLTWPPAIKLGFYALGVILVGLIINSLALWVFCRMOQTETRIYMT 60

QY 61 NLAVADLCLLCTLPVLHSLRDTSTPLCQLSQGIYLTNRVMSISLVTAIADVAVVRH 120
Db 61 NLAVADLCLLCTLPVLHSLRDTSTPLCQLSQGIYLTNRVMSISLVTAIADVAVVRH 120

QY 121 PLRARGLSRPRQAAAVCAVLVWLVIGSLVARWLLGIQGGFCFRTRHFNFSMRPFLGLF 180
Db 121 PLRARGLSRPRQAAAVCAVLVWLVIGSLVARWLLGIQGGFCFRTRHFNFSMRPFLGLF 180

QY 181 YLPLAVVVFCSLKVTALAQRPPTDVGAEATRKAAKRMVWNLVVFVCFPLHVLGTVR 240
Db 181 YLPLAVVVFCSLKVTALAQRPPTDVGAEATRKAAKRMVWNLVVFVCFPLHVLGTVR 240

QY 241 LAVGNACALLETIRRALYITTSKLSANDCCCLDAICYYTMAKEFQASALAVAPRAKAHS 300
Db 241 LAVGNACALLETIRRALYITTSKLSANDCCCLDAICYYTMAKEFQASALAVAPRAKAHS 300

QY 301 QDSLCVTLA 309
Db 301 QDSLCVTLA 309

RESULT 3
Q4ZFV2 HUMAN
ID Q4ZFV2 HUMAN PRELIMINARY; PRT; 309 AA.
AC Q4ZFV2;
DT 13-SEP-2005 (TREMBLrel. 31, Created)
DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update)

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13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
DE Hypothetical protein GPR35.  
GN Name=GPR35;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Haakenson W., Trani L., Schatzkammer K.;  
RA "the sequence of Homo sapiens BAC clone RP11-27M15.";  
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RA Waterston R.H.;  
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RA Waterston R.;  
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP NUCLEOTIDE SEQUENCE.  
RA Wilson R.K.;  
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.  
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).  
CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.  
DR EMBL; AC124862; AAX8945.1; -; Genomic DNA.  
DR InterPro; IPR000276; GPCR\_Rhodpsn.  
DR Pfam; PF00001; 7tm.1; 1.  
DR PRINTS; PS00237; GPCR\_Rhodopsin.  
DR PROSITE; PS00237; G-PROTEIN RECEPTOR\_F1\_1; 1.  
DR PROSITE; PS0262; G-PROTEIN RECEPTOR\_F1\_2; 1.  
KW G-protein coupled receptor; Hypothetical protein; Receptor;  
KW Transducer; Transmembrane.  
SQ SEQUENCE 309 AA; 34072 MW; 97734FB7231B26F0 CRC64;  
  
Query Match 99.3%; Score 1602; DB 2; Length 309;  
Best Local Similarity 99.4%; Pred. No. 4.9e-112;  
Matches 307; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 1 MNGTYNTCGSSDLTPWPAIKLGFAYLVGLVLLGLLNSLALWVFCRCMQQTETRIYMT 60  
DB 1 MNGTYNTCGSSDLTPWPAIKLGFAYLVGLVLLGLLNSLALWVFCRCMQQTETRIYMT 60  
  
QY 61 NLAVADLCCLCTLPFVLSLSDTSTPLCQLSQGIYLTNRYSISLVTAIAVDVAVRH 120  
DB 61 NLAVADLCCLCTLPFVLSLSDTSTPLCQLSQGIYLTNRYSISLVTAIAVDVAVRH 120  
  
QY 121 PLRAGRLSPROAAVCAVLVLTGSLVAVRLVLTGSGGFCFRTRHNFNSMRPPLG 180  
DB 121 PLRAGRLSPROAAVCAVLVLTGSLVAVRLVLTGSGGFCFRTRHNFNSMRPPLG 180  
  
QY 181 YLPLAVVVFCSLKVVTTALAQRPPTDVGOAEATRKARVMWVWVLLVFWVCFPLHVLTVR 240  
DB 181 YLPLAVVVFCSLKVVTTALAQRPPTDVGOAEATRKARVMWVWVLLVFWVCFPLHVLTVR 240  
  
QY 241 LAVGNACALLETIRRALYITSKLSANDCCCLDAICYVMYMAKQFQASALAVAPRAKHK 300  
DB 241 LAVGNACALLETIRRALYITSKLSANDCCCLDAICYVMYMAKQFQASALAVAPRAKHK 300  
  
QY 301 QDSLVCVTLA 309  
DB 301 QDSLVCVTLA 309  
  
RESULT 4  
Q6ZMP9 HUMAN PRELIMINARY; PRT; 394 AA.  
ID Q6ZMP9;  
AC Q6ZMP9;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

Hypothetical protein FLJ16773.  
DE Homo sapiens (Human).  
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Kawakami B., Sugiyama A., Takemoto M., Sugiyama T., Irie R.,  
RA Otsuki T., Sato H., Ota T., Wakamatsu A., Ishii S., Yamamoto J.,  
RA Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K.,  
RA Yamashita H., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,  
RA Wagatsuma M., Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A.,  
RA Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.;  
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.  
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).  
CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.  
DR EMBL; AK131540; BADI8676.1; -; mRNA.  
DR Ensembl; ENSG00000178623; Homo sapiens.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0004872; F:receptor activity; IEA.  
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.  
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.  
DR InterPro; IPR000276; GPCR\_Rhodpsn.  
DR Pfam; PF00001; 7tm.1; 1.  
DR PRINTS; PS00237; GPCR\_Rhodopsin.  
DR PROSITE; PS00237; G-PROTEIN RECEPTOR\_F1\_1; 1.  
DR PROSITE; PS0262; G-PROTEIN RECEPTOR\_F1\_2; 1.  
KW G-protein coupled receptor; Receptor; Transducer; Transmembrane.  
SQ SEQUENCE 394 AA; 43309 MW; 1598FD44BAE4233C CRC64;  
  
Query Match 99.3%; Score 1602; DB 2; Length 394;  
Best Local Similarity 99.4%; Pred. No. 6e-112;  
Matches 307; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 1 MNGTYNTCGSSDLTPWPAIKLGFAYLVGLVLLGLLNSLALWVFCRCMQQTETRIYMT 60  
DB 86 MNGTYNTCGSSDLTPWPAIKLGFAYLVGLVLLGLLNSLALWVFCRCMQQTETRIYMT 145  
  
QY 61 NLAVADLCCLCTLPFVLSLSDTSTPLCQLSQGIYLTNRYSISLVTAIAVDVAVRH 120  
DB 146 NLAVADLCCLCTLPFVLSLSDTSTPLCQLSQGIYLTNRYSISLVTAIAVDVAVRH 205  
  
QY 121 PLRAGRLSPROAAVCAVLVLTGSLVAVRLVLTGSGGFCFRTRHNFNSMRPPLG 180  
DB 206 PLRAGRLSPROAAVCAVLVLTGSLVAVRLVLTGSGGFCFRTRHNFNSMRPPLG 265  
  
QY 181 YLPLAVVVFCSLKVVTTALAQRPPTDVGOAEATRKARVMWVWVLLVFWVCFPLHVLTVR 240  
DB 266 YLPLAVVVFCSLKVVTTALAQRPPTDVGOAEATRKARVMWVWVLLVFWVCFPLHVLTVR 325  
  
QY 241 LAVGNACALLETIRRALYITSKLSANDCCCLDAICYVMYMAKQFQASALAVAPRAKHK 300  
DB 326 LAVGNACALLETIRRALYITSKLSANDCCCLDAICYVMYMAKQFQASALAVAPRAKHK 385  
  
QY 301 QDSLVCVTLA 309  
DB 386 QDSLVCVTLA 394  
  
RESULT 5  
Q4VEN5 HUMAN PRELIMINARY; PRT; 308 AA.  
ID Q4VEN5;  
AC Q4VEN5;  
DT 13-SEP-2005 (TrEMBLrel. 31, Created)  
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)  
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
DE GPR35 protein (Fragment).  
GN Name=GPR35;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TSSUE=G-protein coupled receptors;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards D., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Touchman J.W., Green E.D., Dickinson M.C.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TSSUE=G-protein coupled receptors;
RG NIH MGC Project;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
CC -I- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -I- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
DR EMBL; BC095500; AAH95500.1; -; mRNA.
DR InterPro; IPR000276; GPCR_Rhodopsin.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPS.
DR PROSITE; PS00237; G PROTEIN RECP F1_1; 1.
DR PROSITE; PS00262; G PROTEIN RECP F1_2; 1.
KW G-protein coupled receptor; Receptor; Transducer; Transmembrane.
FT NON_TER 1
FT NON_TER 308
FT NON_TER 308
SQ SEQUENCE 308 AA; 33941 MW; 5791BP9CE7206034 CRC64;
Query Match 98.9%; Score 1597; DB 2; Length 308;
Best Local Similarity 99.4%; Pred. No. 1.le-111;
Matches 306; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 NGTYNTCGSSDLTPWPAIKGLFYAYLGLVLLVGLLNSLALWVFCRMOQWTTTRYMTN 61
DB 1 NGTYNTCGSSDLTPWPAIKGLFYAYLGLVLLVGLLNSLALWVFCRMOQWTTTRYMTN 60
QY 62 LAVADICLCTLPFLVLSLRDTSPTLCSQGIYLTNRVMSISLVATAVDVRYAVRHP 121
DB 61 LAVADICLCTLPFLVLSLRDTSPTLCSQGIYLTNRVMSISLVATAVDVRYAVRHP 120
QY 122 LRARGLSRQAAAVCAVLVVLVIGSILVARWLLGIEGGFCFSTRHFNFSMFPLLGIFY 181
DB 121 LRARGLSRQAAAVCAVLVVLVIGSILVARWLLGIEGGFCFSTRHFNFSMFPLLGIFY 180
QY 182 LPLAVVVFCSLKVTALAPPTDVQGAETRAKAAVMWANLVVVFVCFPLHVLGTVRL 241
DB 181 LPLAVVVFCSLKVTALAPPTDVQGAETRAKAAVMWANLVVVFVCFPLHVLGTVRL 240
QY 242 AVGNWACALLETIRRALYITSLKSDANCCLDAICYYTMAKGFQESALAVAPSAKHSQ 301
DB 241 AVGNWACALLETIRRALYITSLKSDANCCLDAICYYTMAKGFQESALAVAPSAKHSQ 300
QY 302 DSLCVTLA 309
DB 301 DSLCVTLA 308
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RESULT 6
GPR35_MOUSE
ID GPR35_MOUSE STANDARD; PRT; 307 AA.
AC Q9ES90;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE 10-MAY-2005 (Rel. 47, Last annotation update)
DE Probable G-protein coupled receptor 35.
GN Name=Gpr35;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20472315; PubMed=11017071; DOI=10.1038/79876;
RA Horikawa Y., Oda N., Cox N.J., Li X., Orho-Melander M., Hara M.,
RA Hinochio Y., Lindner T.H., Mashima H., Schwarz P.E.H.,
RA del Bosque-Plata L., Horikawa Y., Oda Y., Yoshiuchi I., Colilla S.,
RA Polonsky K.S., Wei S., Concannon P., Iwasaki N., Schulze J.,
RA Baier L.J., Bogardus C., Groop L., Boerwinkle E., Hanis C.L.,
RA Bell G.I.;
RT "Genetic variation in the gene encoding calpain-10 is associated with
RT type 2 diabetes mellitus.";
RL Nat. Genet. 26:163-175(2000).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC STRAIN=C57BL/6J; TISSUE=Mammary gland;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards D., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Touchman J.W., Green E.D., Dickinson M.C.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -I- FUNCTION: Orphan receptor.
CC -I- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -I- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC EMBL; AF200349; AAG18487.1; -; mRNA.
CC EMBL; BC027429; AAH27429.1; -; mRNA.
CC Ensembl; ENSMUSG00000026271; Mus musculus.
CC MGI; MGI:1929509; Gpr35.
CC GO; GO:0016021; C: integral to membrane; TAS.
CC InterPro; IPR000276; GPCR_Rhodopsin.
CC InterPro; IPR002286; P2_puroceptor.
CC Pfam; PF00001; 7tm_1; 1.
CC PRINTS; PR00237; GPCRHHODOPS.
CC PRINTS; PR01157; P2PURNOCPTR.
CC PROSITE; PS00237; G PROTEIN RECP F1_1; 1.
CC PROSITE; PS00262; G PROTEIN RECP F1_2; 1.
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RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,  
RA Saito T., Okazaki Y., Gojibori T., Bono H., Kasukawa T., Saito R.,  
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,  
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,  
RA Schriml L.M., Straubli F., Suzuki R., Tomita M., Wagner L., Washio T.,  
RA Sakai K., Okido T., Furuno M., Bono H., Baldarelli R., Barh G.,  
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
RA Brownstein M.J., Bult C., Fletchmer C., Fujita M., Gariboldi M.,  
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
RA Wynshaw-Boris A., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,  
RA Yushaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,  
RA Hayashizaki Y.;  
RT "Functional annotation of a full-length mouse cDNA collection.";  
RL Nature 409:685-690(2001).  
[3]  
RN NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Bone;  
RA The FANTOM Consortium,  
RA the RIKEN Genome Exploration Research Group Phase I & II Team;  
RT "Analysis of the mouse transcriptome based on functional annotation of  
RT 60,770 full-length cDNAs.";  
RL Nature 420:563-573(2002).  
[4]  
RN NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Bone;  
RX MEDLINE=20493374; PubMed=11042159; DOI=10.1101/gr.145100;  
RA Carninci P., Shibata Y., Hayatsu N., Suganara Y., Shibata K., Itoh M.,  
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;  
RT "Normalization and subtraction of cap-trapper-selected cDNAs to  
RT prepare full-length cDNA libraries for rapid discovery of new genes.";  
RL Genome Res. 10:1617-1630(2000).  
[5]  
RN NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Bone;  
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;  
RA Shibata K., Itoh M., Aizawa K., Nagasaka S., Sasaki N., Carninci P.,  
RA Konno H., Akiyama J., Nishi K., Kiteunai T., Tashiro H., Itoh M.,  
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,  
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,  
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,  
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,  
RA Okazaki Y., Muramatsu M., Inoue Y., Kita A., Hayashizaki Y.;  
RT "RIKEN integrated sequence analysis (RISA) system-384-format  
RT sequencing pipeline with 384 multicapillary sequencer.";  
RL Genome Res. 10:1757-1771(2000).  
[6]  
RN NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Bone;  
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,  
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,  
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,  
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,  
RA Kato H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,  
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,  
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,  
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,  
RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,  
RA Tagawa A., Takahashi F., Takaku-Akaiura S., Takeda Y., Tanaka T.,  
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;  
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).  
CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.  
DR EMBL; AK036503; BAC29453.1; -; mRNA.  
DR MGI; MGI:1929509; Gpr35.  
DR GO; GO:0016021; C:integral to membrane; TAS.  
DR InterPro; IPR000276; GPCR Rhodpen.  
DR InterPro; IPR002286; P2\_purnocptor.  
DR Pfam; PF00001; 7tm\_1; 1.

DR PRINTS; PR00237; GPCRHOPOPSN.  
DR PRINTS; PR01157; P2YFURNOCPTR.  
DR PROSITE; PS00237; G PROTEIN RECP Fl\_1; 1.  
DR PROSITE; PS0262; G PROTEIN RECP Fl\_2; 1.  
KW G-protein coupled receptor; Receptor; Transducer; Transmembrane.  
SQ SEQUENCE 307 AA; 34140 MW; 8EB439AED5F7656 CRC64;  
Query Match 69.8%; Score 1123; DB 2; Length 307;  
Best Local Similarity 71.9%; Pred. No. 3.6e-76;  
Matches 223; Conservative 30; Mismatches 51; Indels 6; Gaps 5;  
QY 1 MNGTYNTGSSDLTWPAPKIGFYAVLGLVGLLNLNLALVFCRCMQWTETRIYMT 60  
DB 1 MNST--TCNST-LTPASVNNFTIYSLALLVGLLNLVALVFCVRMQWTETRIYMT 57  
QY 61 NLAVADLCCLCTLPFVLSLR-DTSDTPLCQLSQGIYLTNRYMSISLVTIAVDYVAVR 119  
DB 58 NLAVADLCCLCSLPFVLSLYSSDTPVQLSQGIYLTNRYMSISLVTIAVDYVAVR 117  
QY 120 HPLRARGLRSPQAAAVCAVLVVLVGLSVARWLLIQEGGFCFRS-TRNFNSMRPPLL 178  
DB 118 HPLRARELRSPQAAAVCAVLVVLVGLSVARWLLIQEGGFCFRS-TRNFNSMRPPLL 177  
QY 179 GFYLPVAVVFCSLKVVTALAQRPPTDVGQAEATKAAARMVWNLVVFVVCPLPLHVLGT 238  
DB 178 GFYLPVAVVFCSLQVVTALAQRPPTDVGQAEATKAAARMVWNLVVFVVCPLPLHVLGT 237  
QY 239 VRLAVGNACALLETIRRALYITSLKSLDANCLDCLDAICYMAYKEFOEASALAVAPRAKAH 298  
DB 238 VQVSLNLTCAARDTFSRALSITGKSLDINCLDCLDAICYMAYKEFOEASALAVAPRAKAH 296  
QY 299 KSQDSLQCVTL 308  
DB 297 KSQDSLQSL 306  
RESULT 9  
Q8BS98\_MOUSE PRELIMINARY; PRT; 307 AA.  
AC Q8BS98;  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Mus musculus 12 days embryo embryonic body between diaphragm region  
DE and neck cDNA, RIKEN full-length enriched library, clone:9430051L15  
DE product:G protein-coupled receptor 35, full insert sequence.  
GN Name=Gpr35;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J;  
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;  
RA Carninci P., Hayashizaki Y.;  
RT "High-efficiency full-length cDNA cloning.";  
RL Meth. Enzymol. 303:19-44(1999).  
[2]  
RN NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J;  
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;  
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
RA Aizawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,  
RA Saito T., Okazaki Y., Gojibori T., Bono H., Kasukawa T., Saito R.,  
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,  
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,  
RA Schriml L.M., Straubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,  
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohetsuki S.,  
 RA Hayashizaki Y.;  
 RA "Functional annotation of a full-length mouse cDNA collection.";  
 RL Nature 409:685-690(2001).  
 RN [3]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J;  
 RC TISSUE=Embryonic body between diaphragm region and neck;  
 RC THE FANTOM Consortium,  
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 RT 60,770 full-length cDNAs";  
 RL Nature 420:563-573(2002).  
 RN [4]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J;  
 RC TISSUE=Embryonic body between diaphragm region and neck;  
 RC MEDLINE=20493374; PubMed=11042159; DOI=10.1101/gr.152600;  
 RX Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,  
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;  
 RA "Normalization and subtraction of cap-trapper-selected cDNAs to  
 RT prepare full-length cDNA libraries for rapid discovery of new genes";  
 RL Genome Res. 10:1617-1630(2000).  
 RN [5]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J;  
 RC TISSUE=Embryonic body between diaphragm region and neck;  
 RC MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;  
 RX Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,  
 RA Konno H., Akiyama J., Nishi K., Kitsuina T., Tashiro H., Itoh M.,  
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,  
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,  
 RA Fujiwaka S., Inoue K., Togawa Y., Iizawa M., Ohara E., Watahiki M.,  
 RA Yoneda Y., Ighikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,  
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;  
 RT "RIKEN integrated sequence analysis (RISA) system-384-format  
 RT sequencing pipeline with 384 multicapillary sequencer.";  
 RL Genome Res. 10:1757-1771(2000).  
 RN [6]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J;  
 RC TISSUE=Embryonic body between diaphragm region and neck;  
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,  
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,  
 RA Horii P., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,  
 RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,  
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,  
 RA Nihi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,  
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,  
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,  
 RA Tagawa A., Takahashi F., Takaku-Akaiura S., Takeda Y., Tanaka T.,  
 RA Tomaru A., Toyota T., Yasunishi A., Muramatsu M., Hayashizaki Y.;  
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).  
 CC -!- SIMILARITY: Belongs to the G-protein coupled receptor-1 family.  
 DR EMBL; AK034870; BAC28861.1; -; mRNA.  
 DR MGI; MGI:1929509; Gpr35.  
 DR GO; GO:0016021; C:integral to membrane; TAS.  
 DR InterPro; IPR000276; GPCR\_Rhodopsn.  
 DR InterPro; IPR002286; P2\_purinceptor.  
 DR Pfam; PF00001; 7tm 1; 1.  
 DR PRINTS; PR00237; GPCR\_Rhodopsn.  
 DR PRINTS; PR01157; P2Y\_Purinceptor.  
 DR PROSITE; PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.

DR PROSITE; PS0262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
 KW G-protein coupled receptor; Receptor; Transducer; Transmembrane.  
 SQ SEQUENCE 307 AA; 34260 MW; 923D02CECB0D70AC CRC64;  
 Query Match 68.7%; Score 1109; DB 2; Length 307;  
 Best Local Similarity 71.3%; Pred. No. 4e-75;  
 Matches 221; Conservative 30; Mismatches 53; Indels 6; Gaps 5;  
 QY 1 MNGTYNTCGSSDLTPWPPAIGLGFVYLVGLVLLGLLNLALWVFCRCMQQWETRIYMT 60  
 DB 1 MNST--TCNST-ITWPAVNNFFIYSALLVLLGLLNSVALWVFCYRMHQWETRIYMT 57  
 QY 61 NLAVADLCCLCTPLFPVLHSLR-DTSDPCLCOLSGIYLTNRYMSISLTAIVADRYAVR 119  
 DB 58 NLAVADLCCLCSLPFVLYSLKYSSTDPVQQLSGIYLTNRYMSISLTAIVADRYAVR 117  
 QY 120 HPLRARGLRPRQAAAVCAVLWLVIGSLVARNLGLOEGGFCPRS-TRNNFNSMRPPLL 178  
 DB 118 HPLRARELRSPQAAAVCAVWLVVITSLVVRMLGMOEGGFCPSQTRNFSTAFSL 177  
 QY 179 GFYLPVAVVFCSLKVVYVTLAQAQPPTDVGQAEATRKAAWVWVWVWVWVWVWVWVWV 238  
 DB 178 GFYLPVAVVFCSLQVVVLSRRPAADVQAEATQKATWVWVWVWVWVWVWVWVWV 237  
 QY 239 VRLAVGNACALLETRIRALYITSKLSANDCLDAICYNNMAKFEQASALAVAPRAK 298  
 DB 238 VQVSLNLTCAARDTFSRALSITGKLSDTNCLDAICYNNMAKFEQAFKATSSNT-PH 296  
 QY 299 KSQDSLCTVL 308  
 DB 297 KSQYSQILSL 306  
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 Q4TAH0\_TETNG  
 ID Q4TAH0\_TETNG PRELIMINARY; PRT; 305 AA.  
 AC Q4TAH0;  
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)  
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)  
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
 DE Chromosome 1 SCAP7335, whole genome shotgun sequence. (Fragment).  
 GN ORFNames=GSTNG0004207001;  
 OS Tetraodon nigroviridis (Green puffer).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
 OC Acanthomorpha; Acanthopterygii; Percomorphs; Tetraodontiformes;  
 OC Tetraodontidae; Tetraodontidae; Tetraodon.  
 OX NCBI\_TaxID=99883;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,  
 RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,  
 RA Nicaud S., Jaffe D., Fisher S., Luthalla G., Dossat C., Segurens B.,  
 RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,  
 RA Anthonard V., Jubin C., Castelli V., Katinka M., Vacherie B.,  
 RA Bismont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,  
 RA Craud C., Duprat S., Brottier P., Coutanceau J.P., Guzy J.,  
 RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,  
 RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,  
 RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,  
 RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,  
 RA Wincker P., Lander E.S., Weissbach J., Roest Crolius H.;  
 RA "Genome duplication in the teleost fish Tetraodon nigroviridis reveals  
 RT the early vertebrate proto-karyotype.";  
 RL Nature 431:946-957(2004).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RG Genoscope; Whitehead Institute Centre for Genome Research;  
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.  
 CC -!- CAUTION: The sequence shown here is derived from an  
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
 CC preliminary data.  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).

[illegible]

RA O'Dowd B.F., Nguyen T., Jung B.P., Marchese A., Cheng R., Heng H.H.Q.,  
RA Kolakowski L.F. Jr., Lynch K.R., George S.R.;  
RT "Cloning and chromosomal mapping of four putative novel human G-  
RT protein-coupled receptor genes";  
RL Gene 187:75-81(1997).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RA Bohm S.K., Khitin L.M., Pavan D.P., Bunnett N.W.;  
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=97366605; PubMed=3223435; DOI=10.1006/bbrc.1997.6895;  
RA Janssens R., Boeynaems J.M., Godart M., Communi D.;  
RT "Cloning of a human heptahelical receptor closely related to the P2Y5  
RT receptor";  
RL Biochem. Biophys. Res. Commun. 236:106-112(1997).  
RN [4]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
RX PubMed=15772651; DOI=10.1038/nature03440;  
RA Ross M.T., Grafham D.V., Coffey A.J., Scherer S., McIlroy K., Muzny D.,  
RA Platzer M., Howell G.R., Burrows C., Bird C.P., Frankish A.,  
RA Lovell F.L., Howe K.L., Ashurst J.L., Fulton R.S., Sudbrak R., Wen G.,  
RA Jones M.C., Hultes M.E., Andrews T.D., Scott C.E., Searle S.,  
RA Ramser J., Whitaker A., Deadman R., Carter N.P., Hunt S.E., Chen R.,  
RA Cree A., Gunaratne P., Havlak P., Hodgson A., Metzker M.L.,  
RA Richards S., Scott G., Steffen D., Sodergren E., Wheeler D.A.,  
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RA Aswell R.I., Babbage A.K., Bagguley C.L., Ballabio A., Banerjee R.,  
RA Barker G.E., Barlow K.F., Barrett I.P., Bates K.N., Beare D.M.,  
RA Beasley H., Beasley O., Beck A., Bethel G., Blechschmidt K., Brady N.,  
RA Bray-Allen S., Bridgeman A.M., Brown A.J., Brown M.J., Bonnin D.,  
RA Bruford E.A., Bunay C., Burch P., Burford D., Burgess J., Burrill W.,  
RA Burton J., Bye J.M., Carder C., Carrel L., Chakko J., Chapman J.C.,  
RA Chavez D., Chen G., Chen Y., Chen Z., Chinault C.,  
RA Ciccodicola A., Clark S.Y., Clarke G., Clee C.M., Clegg S.,  
RA Clerc-Blankenburg K., Clifford K., Cobley V., Cole C.G., Conquer J.S.,  
RA Corby N., Connor R.E., David R., Davies J., Davis C., Davis J.,  
RA Delgado O., Deshazo D., Dhani P., Ding Y., Dinh H., Dodsworth S.,  
RA Draper H., Dugan-Rocha S., Dunham A., Dunn M., Durbin K.J., Dutta I.,  
RA Eades T., Ellwood M., Emery-Cohen A., Errington H., Evans K.L.,  
RA Faulkner L., Francis F., Frankland J., Fraser A.E., Galgoczy P.,  
RA Gilbert J., Gill R., Gloeckner G., Gregory S.G., Gribble S.,  
RA Griffiths C., Grocock R., Gu Y., Gwilliam R., Hamilton C., Hart E.A.,  
RA Hawes A., Heath P.D., Heitmann K., Hennig R., Hernandez J.,  
RA Hinzmann B., Ho S., Hoffs M., Howden P.J., Huckle E.J., Hume J.,  
RA Hunt P.J., Hunt A.R., Isherwood J., Jacob L., Johnson D., Jones S.,  
RA de Jong P.J., Joseph S.S., Keenan S., Kelly S., Kershaw J.K., Khan Z.,  
RA Kioschis P., Klares S., Knights A.J., Koslira A., Kovar-Smith C.,  
RA Laird G.K., Langford C., Lawlor S., Leversha M., Lewis L., Liu W.,  
RA Lloyd C., Lloyd D.M., Louisegh J., Loveland J.E., Lovell J.D.,  
RA Lozano R., Lu J., Lyne R., Ma J., Maheshwari M., Matthews L.H.,  
RA McDowall J., McLaren S., McMurray A., Meidl P., Meitinger T.,  
RA Milne S., Miner G., Mistry S.L., Morgan M., Morris S., Mueller I.,  
RA Mullikin J.C., Nguyen N., Nordiek G., Nyakatura G., O'dell C.N.,  
RA Okwunigbo G., Palmer S., Pandian R., Parker D., Parrish J.,  
RA Pasternak S., Patel D., Pearce A.V., Pearson D.M., Pelan S.E.,  
RA Perez L., Porter K.M., Ramsey Y., Reichwald K., Rhodes S.,  
RA Ridler K.A., Schlössinger D., Schueler M.G., Sehra H.K.,  
RA Shaw-Smith C., Shen H., Sheridan E.M., Shownkeen R., Skuce C.D.,  
RA Smith W.L., Sotheran E.C., Steingrubber H.E., Steward C.A., Storey R.,  
RA Swann R.M., Swarbreck D., Tabor P.E., Taudien S., Taylor T.,  
RA Teague B., Thomas K., Thorpe A., Timms K., Tracey A., Trevanion S.,  
RA Tromans A.C., d'Urso M., Verduzco D., Villanueva D., Waldron L.,  
RA Wall M., Wang Q., Warren J., Warry G.L., Wei X., West A.,  
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RA Williams G., Williams L., Williamson A., Williamson H., Wilming L.,  
RA Woodmansey R.L., Wray P.W., Yen J., Zhang J., Zhou J., Zoghbi H.,

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RA Lehrach H., Meindl A., Minx P.J., Hillier L.W., Willard H.F.,  
RA Wilson R.K., Waterston R.H., Rice C.M., Vaudin M., Coulson A.,  
RA Nelson D.L., Weinstock G., Sulston J.E., Durbin R., Hubbard T.,  
RA Gibbs R.A., Beck S., Rogers J., Bentley D.R.;  
RT "The DNA sequence of the human X chromosome";  
RL Nature 434:325-337(2005).  
RN [6]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].  
RC TISSUE=Brain;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smillius D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -1- TISSUE SPECIFICITY: Not detected in the brain regions thalamus,  
CC putamen, caudate, frontal cortex, pons, hypothalamus and  
CC hippocampus.  
CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.  
CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use as long as its content is in no way modified and this statement is not  
CC removed.  
CC EMBL; U66578; AAC51301.1; -; Genomic DNA.  
CC EMBL; U90323; AAB62087.1; -; Genomic DNA.  
CC EMBL; U90322; AAB62088.1; -; mRNA.  
CC EMBL; AF005419; AAB66322.1; -; Genomic DNA.  
CC EMBL; AY301274; AAP58404.1; -; Genomic DNA.  
CC EMBL; AL590083; CAD18851.1; -; Genomic DNA.  
CC EMBL; BC074722; AAH74722.1; -; mRNA.  
CC PIR; JC5549; JC5549.  
CC HSPF; P34996; 1DDD.  
CC Ensembl; ENSG00000147145; Homo sapiens.  
CC HGNC; HGNC:4478; GPR23.  
CC MIM; 300086; -;  
CC GO; GO:0005887; C:integral to plasma membrane; TAS.  
CC GO; GO:0004930; P:G-protein coupled receptor activity; TAS.  
CC GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; TAS.  
CC InterPro; IPR000276; GPCR\_Rhodopsn.  
CC InterPro; IPR002188; P2Y5\_purinocptor.  
CC Pfam; PF00001; 7tm\_1; 1.  
CC PRINTS; PR00237; GPCR\_Rhodopsn.  
CC PRINTS; PR01067; P2Y5ORPHAN.  
CC PROSITE; PS00237; G-PROTEIN RECEPTOR\_F1\_1; 1.  
CC PROSITE; PS00262; G-PROTEIN RECEPTOR\_F1\_2; 1.  
CC G-protein coupled receptor; Glycophorin; Receptor; Transducer;  
KW Transmembrane. 1 43 Extracellular (Potential).  
FT TOPO\_DOM 1 43  
FT TRANSMEM 44 64 1 (Potential).  
FT TOPO\_DOM 65 73 Cytoplasmic (Potential).  
FT TRANSMEM 74 94 2 (Potential).  
FT TOPO\_DOM 95 112 Extracellular (Potential).  
FT TRANSMEM 113 133 3 (Potential).



GN Name=Gpr23;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridae; Murinae; Mus.  
OC NCBI\_TaxID=10090;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Spinal ganglion;  
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;  
RA Carninci P., Hayashizaki Y.;  
RL "High-efficiency full-length cDNA cloning.";  
RM Meth. Enzymol. 303:19-44(1999).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Spinal ganglion;  
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;  
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamakura I.,  
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,  
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,  
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,  
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,  
RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,  
RA Hayashizaki Y.;  
RL "Functional annotation of a full-length mouse cDNA collection.";  
RM Nature 409:685-690(2001).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Spinal ganglion;  
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;  
RA Carninci P., Shibata Y., Hayatsu N., Sugihara Y., Shibata K., Itoh M.,  
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;  
RL "Normalization and subtraction of cap-trapper-selected cDNAs to  
prepare full-length cDNA libraries for rapid discovery of new genes.";  
RM Genome Res. 10:1617-1630(2000).  
RN [4]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Spinal ganglion;  
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;  
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,  
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,  
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishigami T., Kashiwagi K.,  
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,  
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,  
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,  
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;  
RL "RIKEN integrated sequence analysis (RISA) system-384-format  
sequencing pipeline with 384 multicapillary sequencer.";  
RM Genome Res. 10:1757-1771(2000).  
RN [5]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Spinal ganglion;  
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;  
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,  
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,  
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishigami T., Kashiwagi K.,  
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,  
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,  
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,  
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;  
RL "RIKEN integrated sequence analysis (RISA) system-384-format  
sequencing pipeline with 384 multicapillary sequencer.";  
RM Genome Res. 10:1757-1771(2000).  
RN [6]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Spinal ganglion;  
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,  
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,

RA Hayaashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,  
RA Hori P., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,  
RA Kato H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,  
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,  
RA Nishi K., Nomura K., Numazaki R., Ohno M., Oheato N., Okazaki Y.,  
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,  
RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tegami M.,  
RA Tagawa A., Takahashi F., Takaku-Akashira S., Takeda Y., Tanaka T.,  
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;  
RL Submitter (JUL-2001) to the EMBL/GenBank/DBJ databases.  
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).  
DR EMBL; AK051709; BAC34729.1; -; mRNA.  
DR DR  
DR MG1; MG1:1925384; Gpr23.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0045028; F:purinergic nucleotide receptor activity; G- . . ; IEA.  
DR GO; GO:0004872; F:receptor activity; IEA.  
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.  
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . ; IEA.  
DR GO; GO:0007165; P:signal transduction; IEA.  
DR InterPro; IPR002186; GPCR\_Rhodopsin.  
DR InterPro; IPR002186; P2Y5\_purinceptor.  
DR Pfam; PF00001; 7tm.1.1.  
DR PRINTS; PR00237; GPCR\_Rhodopsin.  
DR PRINTS; PR01067; P2Y5ORPHAN.  
DR PROSITE; PS00237; G PROTEIN RECEPTOR FL1; UNKNOWN\_1.  
DR PROSITE; PS00262; G PROTEIN RECEPTOR FL2; 1.  
DR PROSITE; PS00262; G PROTEIN RECEPTOR FL2; 1.  
DR KW G-protein coupled receptor; Receptor; Transducer; Transmembrane.  
SQ SEQUENCE 370 AA; 41956 MW; AB126842343AE6E1 CRC64;  
Query Match 24.8%; Score 400; DB 2; Length 370;  
Best Local Similarity 34.3%; Pred. No. 5.8e-22;  
Matches 104; Conservative 59; Mismatches 112; Indels 28; Gaps 11;  
Qy 4 TYNTGSSDLTWPAPKIGFY-AVLGVLLVGLLNSLALWVFCRMOQWETRIYMTNL 62  
Db 27 TNNTCIQVDD-----SFKTNLNGAVSVVFLGLTNSASLFFCFMRKMRSETAIFINL 81  
Qy 63 AVADLCILCTLPF-VLHSLR---DTSDDTLCQLSQGLYLTNRYMSISLVTAIAVDYRVAV 118  
Db 82 ALSDLLFVCTLPFKIFYNFNRHWPFGDT-LCKISGTAFLTNIYGSMLFLTCISVDRLAI 140  
Qy 119 RHPRLARGLRSPROAAVCAVLVVLVIGSLVARWLLGQF-----GGCFRSTRHN 169  
Db 141 VYFPRSTRIRTRNSAIVCAGWILVLLNGGISLSTFTNNVNNATTTTCFGEFSEKRWKTY 200  
Qy 170 FNSMR--PPLLGFLVPLAVVVCSSIKVVTALAQRPPTDVQAEAT-RKAARVMANLLVF 226  
Db 201 LSKITIFIEVVGFIPLINVCSSSVLRTL--RKPATLSQIGTKKVKLVKMTYHMAVF 258  
Qy 227 VVCFPLHVLGTLVRLAVGNAC--ALLETTIRRLY-ITSKLSDANCCLDAICYVMKEF 283  
Db 259 VVCFVPYNSVLFYALVRSQAITNCLERFAKIMYPITLCLATLNCNCFDPFIYFTLESF 318  
Qy 284 QEA 286  
Db 319 QKS 321  
RESULT 15  
Q8BLG2 MOUSE  
ID Q8BLG2 MOUSE PRELIMINARY; PRT; 370 AA.  
AC Q8BLG2.  
DT 01-MAR-2003 (TREMBLrel. 23, Created)  
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)  
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
DE Mus musculus 9.5 days embryo parthenogenote cDNA, RIKEN full-length  
DE enriched library, clone:B130055L15 product:P2Y PURINOCEPTOR 9, full  
DE insert sequence.  
GN Name=Gpr23;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridae; Murinae; Mus.



NCBI\_TaxID=10090;  
[1]  
NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Parthenogenote;  
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;  
RA Carninci P., Hayashizaki Y.;  
RT "High-efficiency full-length cDNA cloning.";  
RL Meth. Enzymol. 303:19-44(1999).  
[2]  
NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Parthenogenote;  
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;  
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,  
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
RA Pleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,  
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,  
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,  
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.P.,  
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
RA Lyons P., Marchionni L., Maehima J., Mazzarelli J., Mombaerts P.,  
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,  
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,  
RA Hayashizaki Y.;  
RT "Functional annotation of a full-length mouse cDNA collection.";  
RL Nature 409:685-690(2001).  
[3]  
NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Parthenogenote;  
RA The PANTOM Consortium.  
RA The RIKEN Genome Exploration Research Group Phase I & II Team;  
RT "Analysis of the mouse transcriptome based on functional annotation of  
60,770 full-length cDNAs.";  
RL Nature 420:563-573(2002).  
[4]  
NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Parthenogenote;  
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;  
RA Carninci P., Shibata Y., Hayatsu M., Sugahara Y., Shibata K., Itoh M.,  
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;  
RT "Normalization and subtraction of cap-trapper-selected cDNAs to  
prepare full-length cDNA libraries for rapid discovery of new genes.";  
RL Genome Res. 10:1617-1630(2000).  
[5]  
NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Parthenogenote;  
RX MEDLINE=20630913; PubMed=11076861; DOI=10.1101/gr.152600;  
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,  
RA Konno H., Akiyama J., Nishi K., Kikunai T., Tashiro H., Itoh M.,  
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,  
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,  
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,  
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,  
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;  
RT "RIKEN integrated sequence analysis (RISA) system-384-format  
sequencing pipeline with 384 multicapillary sequencer.";  
RL Genome Res. 10:1757-1771(2000).  
[6]  
NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Parthenogenote;  
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,  
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,  
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,  
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,  
RA Kato H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,  
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,  
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,

RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,  
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,  
RA Tagawa A., Takahashi F., Takaku-Akai H. S., Takeda Y., Tanaka T.,  
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,  
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).  
DR EMBL; AK045289; BAC32299.1; -, mRNA.  
DR Ensembl; ENSMUSG0000049929; Mus musculus.  
DR MGI; MGI:1925384; Gpr23.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0045028; P:purinergic nucleotide receptor activity; G- . . ; IEA.  
DR GO; GO:0004872; P:receptor activity; IEA.  
DR GO; GO:0001584; P:rhodopsin-like receptor activity; IEA.  
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . . ; IEA.  
DR GO; GO:0007165; P:signal transduction; IEA.  
DR InterPro; IPR000276; GPCR\_Rhodopsn.  
DR InterPro; IPR002188; p2y5\_purinceptor.  
DR Pfam; PF00001; 7tm 1; 1.  
DR PRINTS; PR00237; GPCR\_Rhodopsn.  
DR PRINTS; PR01067; P2Y5ORPHAN.  
DR PROSITE; PS00237; G PROTEIN RECP F1\_1; UNKNOWN 1.  
DR PROSITE; PS0262; G PROTEIN RECP F1\_2; 1.  
KW G-protein coupled receptor; Receptor; Transducer; Transmembrane.  
SQ SEQUENCE 370 AA, 41872 MW, 0E4C79FEDFD32050 CRC64;  
Query Match 24.3%; Score 392; DB 2; Length 370;  
Best Local Similarity 34.5%; Pred. No. 2.3e-21;  
Matches 97; Conservative 59; Mismatches 103; Indels 22; Gaps 9;  
QY 25 AVIGLVLLVGLGLLSLALWVFCRMOQWTEIRYMTNLAVADLCCLCTLPF-VLHSLR-- 81  
DB 44 AVISVVFILGLITSSASLFFVFCFRMKMRSEFAIFITNLALSLLPVCPLPPKIFNFRH 103  
QY 82 -DTSDTPLCQLSQGIYLTNRNYSISLVTAIAVDYVAVVHPLRGLRSPROAAAVCAVL 140  
DB 104 WFPQGT-LCKISGTAFNLNYGSMPLPLTCISVDREPLAIVYPPRSRTIRTRNSAIVCAGV 162  
QY 141 WVLVIGSLVARWLLGIQE-----GGPCFRSTRHNFNSMR--PPLIGLYPLAVVVF 189  
DB 163 WILVLSGGIGSASLFTSTNVNNATTTCPGFSKRVKTYLSKITIFIEVVGVFIPLILNVS 222  
QY 190 CSLKVVVTAALQRPPTDVGQAEAT-RKAARMVWNLVVFVVCPLPLHVGITVRLAVGMNAC 248  
DB 223 CSSVVLRLTL--RKPATLSQIGTNKKVKLKMITHMAVVFVVCVPSVNLFLYLVRSQAI 280  
QY 249 --ALLETTIRRLY-ITSKLSANCCCLDAICYYMYMAKBFQEA 286  
DB 281 TWCLLERFAKIMYPITLCATLNCPPDPPIYYFTLESFQKS 321

Search completed: February 9, 2006, 01:00:17  
Job time : 168.5 secs



GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: February 9, 2006, 00:47:19 ; Search time 214.5 Seconds  
(without alignments)  
632.951 Million cell updates/sec

Title: US-10-083-168-85

Perfect score: 1615

Sequence: 1 MNGTYTCGSSDLTWPPAIK.....AVAPRAKHKQSDSLCVTLA 309

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A Geneseq 21.\*

- 1: Geneseqp1980s.\*
- 2: Geneseqp1990s.\*
- 3: Geneseqp2000s.\*
- 4: Geneseqp2001s.\*
- 5: Geneseqp2002s.\*
- 6: Geneseqp2003as.\*
- 7: Geneseqp2003bs.\*
- 8: Geneseqp2004s.\*
- 9: Geneseqp2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description        |
|------------|-------|-------------|--------|----|--------------------|
| 1          | 1615  | 100.0       | 309    | 5  | ABG95172 Human GPC |
| 2          | 1609  | 99.6        | 309    | 3  | AAY79576 Human G p |
| 3          | 1609  | 99.6        | 309    | 5  | ABG95159 Human GPC |
| 4          | 1609  | 99.6        | 309    | 6  | ABP82002 Human G p |
| 5          | 1609  | 99.6        | 309    | 7  | ADB67656 Human G p |
| 6          | 1609  | 99.6        | 309    | 8  | ADO29394 Human GPC |
| 7          | 1609  | 99.6        | 309    | 8  | ADO78094 Human GPC |
| 8          | 1609  | 99.6        | 309    | 9  | ADV73203 Human col |
| 9          | 1609  | 99.6        | 309    | 9  | AEB15039 Human GPC |
| 10         | 1603  | 99.3        | 309    | 3  | AAY69989 Human rec |
| 11         | 1603  | 99.3        | 309    | 7  | ADP70461 Orphan re |
| 12         | 1601  | 99.1        | 309    | 7  | ADF50511 Human GPC |
| 13         | 1597  | 98.9        | 309    | 3  | AAY58645 Human G-p |
| 14         | 1597  | 98.9        | 309    | 6  | ADA84069 Human GPC |
| 15         | 1597  | 98.9        | 394    | 8  | ADO78095 Human GPC |
| 16         | 1597  | 98.9        | 394    | 8  | ADR10454 Human pro |
| 17         | 1377  | 85.3        | 286    | 8  | ADP29765 Human sec |
| 18         | 1123  | 65.5        | 307    | 8  | ADO29395 Mouse GPC |
| 19         | 401   | 24.8        | 370    | 2  | AAW62597 Human 7-t |
| 20         | 401   | 24.8        | 370    | 5  | ABP61511 Human NF- |
| 21         | 401   | 24.8        | 370    | 6  | ABG73513 Human p2y |
| 22         | 401   | 24.8        | 370    | 6  | ABP81870 Human G p |
| 23         | 401   | 24.8        | 370    | 7  | ADH69286 Human pur |
| 24         | 401   | 24.8        | 370    | 8  | ADF91778 Human p2y |

|    |       |      |     |   |          |                    |
|----|-------|------|-----|---|----------|--------------------|
| 25 | 401   | 24.8 | 370 | 8 | ADO29049 | Ado29049 Human nov |
| 26 | 401   | 24.8 | 370 | 8 | ADQ88244 | Adq88244 Human 241 |
| 27 | 401   | 24.8 | 370 | 8 | ADQ81575 | Adq81575 Human iys |
| 28 | 401   | 24.8 | 370 | 8 | ADS84260 | Ads84260 Human G p |
| 29 | 401   | 24.8 | 370 | 9 | ADV35123 | Adv35123 Human tra |
| 30 | 401   | 24.8 | 608 | 7 | ADF70491 | Adf70491 Orphan re |
| 31 | 400   | 24.8 | 370 | 7 | ADH69285 | Adh69285 Human pur |
| 32 | 400   | 24.8 | 370 | 8 | ADF91777 | Adf91777 Human p2y |
| 33 | 396   | 24.5 | 370 | 8 | ADO29050 | Ado29050 Mouse nov |
| 34 | 391   | 24.2 | 370 | 5 | ABP61510 | Abp61510 Human NF- |
| 35 | 389   | 24.1 | 368 | 8 | ADS84259 | Ads84259 Human G p |
| 36 | 388   | 24.0 | 327 | 8 | ADO29415 | Ado29415 Mouse GPC |
| 37 | 382.5 | 23.7 | 363 | 9 | ADM44804 | Adm44804 Human RUP |
| 38 | 382.5 | 23.7 | 363 | 9 | ADM44778 | Adm44778 Human EPA |
| 39 | 382.5 | 23.7 | 363 | 9 | AEB20962 | Aeb20962 Human RUP |
| 40 | 381.5 | 23.6 | 363 | 9 | ADM44818 | Adm44818 Human RUP |
| 41 | 381.5 | 23.6 | 363 | 9 | ADM44796 | Adm44796 Human RUP |
| 42 | 380.5 | 23.6 | 363 | 9 | ADM44807 | Adm44807 Human RUP |
| 43 | 379.5 | 23.5 | 363 | 9 | ADM44802 | Adm44802 Human RUP |
| 44 | 378.5 | 23.4 | 363 | 9 | ADM44810 | Adm44810 Human RUP |
| 45 | 378.5 | 23.4 | 363 | 9 | ADM44805 | Adm44805 Human RUP |

#### ALIGNMENTS

##### RESULT 1

ABG95172

ID ABG95172 standard; protein; 309 AA.

XX AC ABG95172;

XX AC

DT 04-DEC-2002 (first entry)

XX DT

DE Human GPCR GPR35 mutant A216K.

XX DE

XX KW Human; transmembrane receptor; G-protein coupled receptor; GPCR; allergy;

XX KW hypertensive; reflux disease; depression; migraine; schizophrenia; ulcer;

XX KW psychototic disorder; asthma; bronchospasm; anaesthesia;

XX KW myocardial infarction; MI; stroke; glaucoma; anxiety;

XX KW prostatic hypertrophy; epilepsy; prostate cancer; rhinitis; angina;

XX KW prostatic hypertrophy; receptor; mutant; mutin.

XX OS Homo sapiens.

OS Synthetic.

XX OS

XX PN WO200268600-A2.

XX PN

XX PD 06-SEP-2002.

XX PD

XX XX 26-FEB-2002; 2002WO-US005625.

XX XX

XX PR 26-FEB-2001; 2001US-0271913P.

XX PR

XX XX (AREN-) ARENA PHARM INC.

XX XX

XX FI Liaw CW, Chalmers DT, Behan DP, Maciejewski-Lenior D, Leonard JN;

XX FI Lin I, Ortuno D;

XX XX WPI; 2002-706980/76.

XX DR N-PSDB; ABS73401.

XX DR

XX XX New human G-protein coupled receptor (GPCR), useful for screening agonist

XX XX or inverse agonist compounds for treating diseases associated with GPCR.

XX PS Example 2; Page 189-190; 201pp; English.

XX PS

XX CC The present invention relates to transmembrane receptors, particularly

XX CC endogenous human G-protein coupled receptors (GPCRs), mutant (non-

XX CC endogenous) versions of the GPCRs, and the polynucleotide sequences

XX CC encoding them. The GPCRs are useful for screening agonist or inverse

XX CC agonist compounds for treating diseases associated with GPCR. Diseases

XX CC that can be treated with such compounds include allergies, hypertension,

XX CC

CC reflux disease, depression, migraine, schizophrenia, ulcers, psychotic  
CC disorders, asthma, bronchospasm, anaesthesia, myocardial infarction (MI),  
CC stroke, glaucoma, prostatic hyperplasia, epilepsy, prostate cancer,  
CC anxiety, prostatic hypertrophy, rhinitis, and angina. The present  
CC sequence represents a mutant human GPCR  
XX  
SQ Sequence 309 AA;

Query Match 100.0%; Score 1615; DB 5; Length 309;  
Best Local Similarity 100.0%; Pred. No. 2.6e-168;  
Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNGTYNTCGSSDLTWPPAIKLGFAVYLVGLVLLGLLNSLALWVFCRMOQWETETRIYMT 60  
DB 1 MNGTYNTCGSSDLTWPPAIKLGFAVYLVGLVLLGLLNSLALWVFCRMOQWETETRIYMT 60

QY 61 NLAVADLCCLCTLPFVHLHSRLDTSPTPLCQLSQGIYLTNRYMSISLVTAIAVDVRYAVRH 120  
DB 61 NLAVADLCCLCTLPFVHLHSRLDTSPTPLCQLSQGIYLTNRYMSISLVTAIAVDVRYAVRH 120

QY 121 PLRARGLRSPROAAAVCAVLWLVIGSLVARWLLGIOEGGFCFRSTRHNFNSMRPPLG 180  
DB 121 PLRARGLRSPROAAAVCAVLWLVIGSLVARWLLGIOEGGFCFRSTRHNFNSMRPPLG 180

QY 181 YLPLAVVVFCSLKVVTALAQRPTDVGOAEATRKAKRWANLLVFPVFCPLPHVGLTVR 240  
DB 181 YLPLAVVVFCSLKVVTALAQRPTDVGOAEATRKAKRWANLLVFPVFCPLPHVGLTVR 240

QY 241 LAVGNACALLETIRRALYITSKLSANCCLDIAICYYMAKEFQASALAVAPRAKAHS 300  
DB 241 LAVGNACALLETIRRALYITSKLSANCCLDIAICYYMAKEFQASALAVAPRAKAHS 300

QY 301 QDSLVCVTLA 309  
DB 301 QDSLVCVTLA 309

RESULT 2  
ID AAY79576 standard; protein; 309 AA.  
XX  
AC AAY79576;  
XX  
DT 15-AUG-2000 (first entry)  
XX  
DE Human G protein coupled receptor GPR35.  
XX  
KW GPR35; G protein coupled receptor; human; NIDDM1;  
KW non-insulin-dependent diabetes mellitus; CAPN10 gene; calpain 10;  
KW diagnosis; therapy.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 174 /note= "encoded by GCG"  
FT Misc-difference 294 /note= "encoded by AGT"  
XX  
PN WO200023603-A2.  
XX  
PD 27-APR-2000.  
XX  
PF 21-OCT-1999; 99WO-US024890.  
XX  
PR 21-OCT-1998; 98US-0105052P.  
PR 13-MAY-1999; 99US-0134175P.  
XX  
PA (ARCH-) ARCH DEV CORP.  
PA (TEXA) UNIV OF TEXAS SYSTEM.  
XX  
PI Polonsky KS, Horikawa Y, Oda N, Sreenan S, Zhou Y, Otani K;  
PI Hanis CL, Bell GI, Cox NJ;

XX  
DR WPI; 2000-339702/29.  
DR N-PSDB; AAA27485, AAY79574, AAY79576.  
XX  
PT Method for screening for type 2 diabetes mellitus comprises detecting a  
PT polymorphism in a calpain encoding nucleic acid segment or a protease-  
PT encoding nucleic acid segment.  
XX  
PS Claim 75; Page 237-238; 257pp; English.  
XX  
CC The present sequence is that of the human gene encoding G protein coupled  
CC receptor, GPR35 as deduced from a composite cDNA (see AAA27485). The  
CC sequence of GPR35 is similar to that of a putative purinoceptor P2Y9  
CC (34.1% identity) suggesting that APP or other nucleotide is its ligand.  
CC GPR35 mRNA was detected in all adult and foetal tissues examined with  
CC relatively higher levels in adult lung, small intestine, colon and  
CC stomach. In these tissues, there are 2 major transcripts of 2.4 and 4.4  
CC kb, whereas in skeletal muscle there is a single transcript of 9.4 kb.  
CC The GPR35 gene is located in a 49,136 bp region (see AAA27475) within the  
CC NIDDM1 region of human chromosome 2. This region also includes the CAPN10  
CC gene, which encodes a novel calpain-like cysteine protease, designated  
CC calpain 10. Mutations in the CAPN10 gene are responsible for  
CC susceptibility to type 2 diabetes. Claimed methods for screening for a  
CC propensity for type 2 diabetes mellitus are based on detection of a  
CC polymorphism in a calpain encoding nucleic acid. Methods are also claimed  
CC for identifying modulators of calpain activity, and using these  
CC modulators to treat diabetes, in particular through the regulation of an  
CC insulin secretory response or insulin mediated glucose transport  
XX  
SQ Sequence 309 AA;

Query Match 99.6%; Score 1609; DB 3; Length 309;  
Best Local Similarity 99.7%; Pred. No. 1.2e-167;  
Matches 308; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNGTYNTCGSSDLTWPPAIKLGFAVYLVGLVLLGLLNSLALWVFCRMOQWETETRIYMT 60  
DB 1 MNGTYNTCGSSDLTWPPAIKLGFAVYLVGLVLLGLLNSLALWVFCRMOQWETETRIYMT 60

QY 61 NLAVADLCCLCTLPFVHLHSRLDTSPTPLCQLSQGIYLTNRYMSISLVTAIAVDVRYAVRH 120  
DB 61 NLAVADLCCLCTLPFVHLHSRLDTSPTPLCQLSQGIYLTNRYMSISLVTAIAVDVRYAVRH 120

QY 121 PLRARGLRSPROAAAVCAVLWLVIGSLVARWLLGIOEGGFCFRSTRHNFNSMRPPLG 180  
DB 121 PLRARGLRSPROAAAVCAVLWLVIGSLVARWLLGIOEGGFCFRSTRHNFNSMRPPLG 180

QY 181 YLPLAVVVFCSLKVVTALAQRPTDVGOAEATRKAKRWANLLVFPVFCPLPHVGLTVR 240  
DB 181 YLPLAVVVFCSLKVVTALAQRPTDVGOAEATRKAKRWANLLVFPVFCPLPHVGLTVR 240

QY 241 LAVGNACALLETIRRALYITSKLSANCCLDIAICYYMAKEFQASALAVAPRAKAHS 300  
DB 241 LAVGNACALLETIRRALYITSKLSANCCLDIAICYYMAKEFQASALAVAPRAKAHS 300

QY 301 QDSLVCVTLA 309  
DB 301 QDSLVCVTLA 309

RESULT 3  
ABG95159  
ID ABG95159 standard; protein; 309 AA.  
XX  
AC ABG95159;  
XX  
DT 04-DEC-2002 (first entry)  
XX  
DE Human GPCR GPR35.  
XX  
KW Human; transmembrane receptor; G-protein coupled receptor; GPCR; allergy;  
KW hypertension; reflux disease; depression; migraine; schizophrenia; ulcer;  
KW psychotic disorder; asthma; bronchospasm; anaesthesia;

KW myocardial infarction; MI; stroke; glaucoma; anxiety;  
KW prostatic hyperplasia; epilepsy; prostate cancer; rhinitis; angina;  
KW prostatic hypertrophy; receptor.  
XX  
OS Homo sapiens.  
XX  
XX WO200268600-A2.  
XX  
XX 06-SEP-2002.  
XX  
XX 26-FEB-2002; 2002WO-US005625.  
XX  
XX 26-FEB-2001; 2001US-0271913P.  
XX  
XX (AREN-) ARENA PHARM INC.  
XX  
XX Liaw CW, Chalmers DT, Behan DP, Maciejewski-Lenior D, Leonard JN;  
PI Lin I, Ortuno D;  
XX  
XX WPI; 2002-706980/76.  
XX  
XX N-PSDB; ABS73345.  
XX  
XX New human G-protein coupled receptor (GPCR), useful for screening agonist  
PT or inverse agonist compounds for treating diseases associated with GPCR.  
XX  
XX Claim 29; Page 128-130; 201pp; English.  
XX  
XX The present invention relates to transmembrane receptors, particularly  
CC endogenous human G-protein coupled receptors (GPCRs), mutant (non-  
CC endogenous) versions of the GPCRs, and the polynucleotide sequences  
CC encoding them. The GPCRs are useful for screening agonist or inverse  
CC agonist compounds for treating diseases associated with GPCR. Diseases  
CC that can be treated with such compounds include allergies, hypertension,  
CC reflux disease, depression, migraine, schizophrenia, ulcers, psychotic  
CC disorders, asthma, bronchospasm, anaesthesia, myocardial infarction (MI),  
CC stroke, glaucoma, prostatic hyperplasia, epilepsy, prostate cancer,  
CC anxiety, prostatic hypertrophy, rhinitis, and angina. The present  
CC sequence represents an endogenous human GPCR  
XX  
XX Sequence 309 AA;

Query Match 99.6%; Score 1609; DB 5; Length 309;  
Best Local Similarity 99.7%; Pred. No. 1.2e-167;  
Matches 308; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 MNGTYNTCGSSDLTWPPAIKLGFYAYLGVLLVGLLLNSLALWVFCRMOQWTETRIYMT 60  
DB 1 MNGTYNTCGSSDLTWPPAIKLGFYAYLGVLLVGLLLNSLALWVFCRMOQWTETRIYMT 60  
QY 61 NLAVADCLLCTLPVFLHSLRSDTPIQLSQGIYLTNRYMSISLVTAIAVDVAVVRH 120  
DB 61 NLAVADCLLCTLPVFLHSLRSDTPIQLSQGIYLTNRYMSISLVTAIAVDVAVVRH 120  
QY 121 PLRAGLSRPROAAVCAVLVVLVIGSLVARMLLGIQGGFCFRTRNFNSMRPPLGFG 180  
DB 121 PLRAGLSRPROAAVCAVLVVLVIGSLVARMLLGIQGGFCFRTRNFNSMRPPLGFG 180  
QY 181 YLPLAVVFCSLKVVYLTALAQRPPTDVQGAETFRKARVMWVNLVYVVCFFDPLHYGLTVR 240  
DB 181 YLPLAVVFCSLKVVYLTALAQRPPTDVQGAETFRKARVMWVNLVYVVCFFDPLHYGLTVR 240  
QY 241 LAVGNACALLTIRRALYITSKLSDANCCLDIAICYTMAKFEQASALAVAPRAKAHKS 300  
DB 241 LAVGNACALLTIRRALYITSKLSDANCCLDIAICYTMAKFEQASALAVAPRAKAHKS 300  
QY 301 QDSLCVTLA 309  
DB 301 QDSLCVTLA 309

RESULT 4  
ABP82002  
ID ABP82002 standard; protein; 309 AA.

XX  
AC ABP82002;  
XX  
DT 04-MAR-2003 (first entry)  
XX  
DE Human G protein-coupled receptor GPR35 protein SEQ ID NO:492.  
XX  
XX G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;  
KW G protein-coupled receptor modulator; antibody; immune-related disease;  
KW growth-related disease; cell regeneration-related disease; AIDS; cancer;  
KW immunological-related cell proliferative disease; autoimmune disease;  
KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;  
KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;  
KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;  
KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;  
KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;  
KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;  
KW ulcer.  
XX  
XX Homo sapiens.  
OS  
XX WO200261087-A2.  
PN  
XX 08-AUG-2002.  
PD  
XX 19-DEC-2001; 2001WO-US050107.  
XX  
XX 19-DEC-2000; 2000US-0257144P.  
PR  
XX (LIFE-) LIFESPAN BIOSCIENCES INC.  
PA  
XX Burmer GC, Roush CL, Brown JP;  
PI  
XX WPI; 2003-046718/04.  
XX  
XX N-PSDB; ABZ42852.  
DR  
XX New isolated antigenic peptides e.g., for G protein-coupled receptors  
PT (GPCR), useful for diagnosing and designing drugs for treating conditions  
PT in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or  
PT autoimmune diseases.  
PT  
XX Disclosure; Fig 1; 523pp; English.  
PS  
XX The present invention describes antigenic peptides (I) comprising: (a)  
XX any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino  
CC acids. Also described: (1) an assay for the detection of a particular G  
CC protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;  
CC and (2) an isolated antibody having high specificity and high affinity or  
CC avidity for a particular GPCR. (I) can be used as GPCR modulators and in  
CC gene therapy. The antigenic peptides for GPCRs are useful in detecting an  
CC antibody against a particular GPCR, and in the production of specific  
CC antibodies. The peptides and antibodies are also useful for detecting the  
CC presence or absence of corresponding GPCRs. The antigenic peptides for  
CC GPCRs and antibodies are useful for diagnosing and designing drugs for  
CC treating immune-related diseases, growth-related diseases, cell  
CC regeneration-related diseases, immunological-related cell proliferative  
CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,  
CC atherosclerosis, bacterial, fungal, protozoan or viral infections,  
CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute  
CC inflammation, allergies, Crohn's disease, diabetes, graft versus host  
CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,  
CC anxiety, depression, schizophrenia, dementia, mental retardation, memory  
CC loss, epilepsy, asthma, tuberculosis, obesity, hypertension,  
CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or  
CC any other disorder in which GPCRs are involved. The antibodies may be  
CC used in immunoassays and immunodiagnosis. ABZ42523 to ABZ42869 encode  
CC GPCR proteins given in ABP81675 to ABP82018, which are used in the  
CC exemplification of the present invention  
XX  
XX Sequence 309 AA;

Query Match 99.6%; Score 1609; DB 6; Length 309;  
Best Local Similarity 99.7%; Pred. No. 1.2e-167;

Matches 308; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNGTYNTCGSSDLTPWPAIKLGFYAYLVGLVLLVGLLNSLALWVFCRMOQWTTETRIYMT 60  
 DB 1 MNGTYNTCGSSDLTPWPAIKLGFYAYLVGLVLLVGLLNSLALWVFCRMOQWTTETRIYMT 60  
 QY 61 NLAVADLCLLCTLPFVLSLRDTSPTPLCQLSGIYLTNRYSISLVTAIAVDVYAVRH 120  
 DB 61 NLAVADLCLLCTLPFVLSLRDTSPTPLCQLSGIYLTNRYSISLVTAIAVDVYAVRH 120  
 QY 121 PLRARGLSRPRQAAAVCAVLWLVIGSLVARMLLGIQEGGFCFRSTRHNFNSRFPPLG 180  
 DB 121 PLRARGLSRPRQAAAVCAVLWLVIGSLVARMLLGIQEGGFCFRSTRHNFNSRFPPLG 180  
 QY 181 YLPLAVVFCSLKVVTALAQRPTDVGQAEATRKAKRMVWVANLLVFWVCFPLHVGLT 240  
 DB 181 YLPLAVVFCSLKVVTALAQRPTDVGQAEATRKAKRMVWVANLLVFWVCFPLHVGLT 240  
 QY 241 LAVGNACALLETTIRRALYITSKLSDANCLDAICYNNMAKFOEASALAVAPRAKAHKS 300  
 DB 241 LAVGNACALLETTIRRALYITSKLSDANCLDAICYNNMAKFOEASALAVAPRAKAHKS 300  
 QY 301 QDSLVCVTLA 309  
 DB 301 QDSLVCVTLA 309

## RESULT 5

ADB67656  
 ID ADB67656 standard; protein; 309 AA.  
 AC ADB67656;  
 XX  
 DT 04-DEC-2003 (first entry)  
 DE Human G protein-coupled receptor 35, SEQ ID 25.  
 XX  
 KW Cardiant; Gene therapy; heart failure; human;  
 KW G protein-coupled receptor 35; receptor.  
 XX  
 OS Homo sapiens.  
 PN WO2003072824-A1.  
 XX  
 PD 04-SEP-2003.  
 PF 27-FEB-2003; 2003WO-JP002228.  
 XX  
 PR 28-FEB-2002; 2002JP-00054388.  
 PR 15-APR-2002; 2002JP-00112228.  
 XX  
 PA (SANY ) SANKYO CO LTD.  
 XX  
 PI Kitakaze M, Takashima S, Asakura M, Isomura T, Furukawa H;  
 PI Koishi R, Nakamaru K;  
 XX  
 DR WPI; 2003-679959/64.  
 DR N-PSDB; ADB67672.  
 XX  
 PT Predicting pathological conditions in heart failure using marker genes  
 and proteins.  
 XX  
 PS Claim 1; Page 111-113; 137pp; Japanese.  
 CC The present invention relates to a method for predicting pathological  
 conditions in heart failure using expression of one of 17 gene sequences  
 (ADB67663-ADB67678); or protein sequences encoded by the genes (ADB67648-  
 ADB67662). The proteins and genes are useful for diagnosis, treatment and  
 prevention of heart failure.  
 CC  
 XX  
 SQ Sequence 309 AA; 99.6%; Score 1609; DB 7; Length 309;

Best Local Similarity 99.7%; Pred. No. 1.2e-167;  
 Matches 308; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNGTYNTCGSSDLTPWPAIKLGFYAYLVGLVLLVGLLNSLALWVFCRMOQWTTETRIYMT 60  
 DB 1 MNGTYNTCGSSDLTPWPAIKLGFYAYLVGLVLLVGLLNSLALWVFCRMOQWTTETRIYMT 60  
 QY 61 NLAVADLCLLCTLPFVLSLRDTSPTPLCQLSGIYLTNRYSISLVTAIAVDVYAVRH 120  
 DB 61 NLAVADLCLLCTLPFVLSLRDTSPTPLCQLSGIYLTNRYSISLVTAIAVDVYAVRH 120  
 QY 121 PLRARGLSRPRQAAAVCAVLWLVIGSLVARMLLGIQEGGFCFRSTRHNFNSRFPPLG 180  
 DB 121 PLRARGLSRPRQAAAVCAVLWLVIGSLVARMLLGIQEGGFCFRSTRHNFNSRFPPLG 180  
 QY 181 YLPLAVVFCSLKVVTALAQRPTDVGQAEATRKAKRMVWVANLLVFWVCFPLHVGLT 240  
 DB 181 YLPLAVVFCSLKVVTALAQRPTDVGQAEATRKAKRMVWVANLLVFWVCFPLHVGLT 240  
 QY 241 LAVGNACALLETTIRRALYITSKLSDANCLDAICYNNMAKFOEASALAVAPRAKAHKS 300  
 DB 241 LAVGNACALLETTIRRALYITSKLSDANCLDAICYNNMAKFOEASALAVAPRAKAHKS 300  
 QY 301 QDSLVCVTLA 309  
 DB 301 QDSLVCVTLA 309

## RESULT 6

ADO29394  
 ID ADO29394 standard; protein; 309 AA.  
 AC ADO29394;  
 XX  
 DT 29-JUL-2004 (first entry)  
 DE Human GPCR GPR35, SEQ ID NO:496.  
 XX  
 KW G protein-coupled receptor; GPCR; drug screening; diagnosis;  
 KW transgenic mouse; neurological disorder; adrenal gland disorder;  
 KW colon disorder; intestinal disorder; cardiovascular disorder;  
 KW muscular disorder; blood disorder; immune disorder; bone disorder;  
 KW joint disorder; metabolic disorder; nutritive disorder; cancer;  
 KW kidney disorder; liver disorder; lung disorder; breast disorder;  
 KW ovary disorder; uterus disorder; prostate disorder; testis disorder;  
 KW skin disorder; stomach disorder; pancreas disorder; spleen disorder;  
 KW thymus disorder; thyroid disorder; antiparkinsonian; antimanic;  
 KW cytostatic; antiinflammatory; vasotropic; antianginal; antiarrhythmic;  
 KW CNS; central nervous system; respiratory; antidiarrhoeic; antidiabetic;  
 KW virucide; hepatotropic; antibacterial; antianaemic; antiseborrhoeic;  
 KW dermatological; antitumor; antithyroid; antiallergic; anorectic;  
 KW immunosuppressive; nephrotropic; gene therapy; GPCR modulator; human;  
 KW receptor.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2004040000-A2.  
 XX  
 PD 13-MAY-2004.  
 XX  
 PF 09-SEP-2003; 2003WO-US028226.  
 XX  
 PR 09-SEP-2002; 2002US-0409303P.  
 PR 09-APR-2003; 2003US-0461329P.  
 XX  
 PA (PRIM-) PRIMAL INC.  
 XX  
 PI Gaitanaris GA, Bergmann JE, Gragerov A, Hohmann J, Li F;  
 PI Madisen L, McIlwain KL, Pavlova MN, Vassilatis D, Zeng H;  
 XX  
 DR WPI; 2004-390329/36.  
 DR N-PSDB; ADO29916.

PT Novel mammalian G protein coupled receptors, useful for identifying  
PT compounds that modulates diagnosing and treating disease condition  
PT associated with GPCR dysfunction e.g. autoimmune diseases, angina  
PT pectoris, Parkinson's disease.

PS Claim 151; SEQ ID NO 496; 542pp; English.

XX The invention relates to human and mouse G protein-coupled receptors  
CC (GPCRs) and nucleic acids encoding them. The invention also relates to  
CC sequences at least 90% identical to the GPCR proteins and nucleic acids  
CC of the invention; methods of treating, preventing or diagnosing diseases  
CC associated with GPCRs of the invention; methods of screening for  
CC compounds useful in the treatment of GPCR-related diseases; a transgenic  
CC mouse comprising a GPCR gene of the invention; a mouse comprising a  
CC mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived  
CC from the transgenic mice; kits comprising several mice, each of which has  
CC a mutation in a different GPCR gene of the invention; and kits comprising  
CC probes which hybridise to GPCR polynucleotides of the invention. The  
CC invention further discloses variants of the GPCR polypeptides and vectors  
CC comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may  
CC be used in the diagnosis, treatment or prevention of a wide variety of  
CC diseases including neurological disorders (e.g., Alzheimer's disease,  
CC depression, diabetic neuropathy, Parkinson's disease or schizophrenia);  
CC disorders of the adrenal gland; disorders of the colon or intestine  
CC (e.g., Crohn's disease, diarrhoea, food poisoning or irritable bowel  
CC syndrome); cardiovascular disorders (e.g., angina, cardiac arrhythmia or  
CC myocardial infarction); muscular disorders; blood disorders (e.g.,  
CC anaemia or leukaemia); immune disorders (e.g., autoimmune disorders or  
CC AIDS); bone and joint disorders (e.g., osteoarthritis, rheumatoid  
CC arthritis, gout or osteoporosis); metabolic or nutritive disorders (e.g.,  
CC obesity, enzyme deficiency-related diseases or vitamin deficiency-related  
CC diseases); and disorders of the kidney, liver, lung, breast, ovary,  
CC uterus, prostate, testis, skin, stomach, pancreas, spleen, thymus and  
CC thyroid (e.g., cancers). The present sequence represents a GPCR of the  
CC invention. Note: The full sequence data for this patent did not form part  
CC of the printed specification; those sequences not shown were obtained in  
CC electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences.

XX Sequence 309 AA;

Query Match 99.6%; Score 1609; DB 8; Length 309;  
Best Local Similarity 99.7%; Pred. No. 1.2e-167;  
Matches 308; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 MNGTYNTCGSSDLTWPPAIIKLGFYAYLVGLVLLGLLNSLALWVFCRMOQTETRIYMT 60  
DB 1 MNGTYNTCGSSDLTWPPAIIKLGFYAYLVGLVLLGLLNSLALWVFCRMOQTETRIYMT 60  
QY 61 NLAVADLCLLCTLPFVLSLRDSTPLCQLSQGIYLTNRNYSISLVTAIAVDVAVRH 120  
DB 61 NLAVADLCLLCTLPFVLSLRDSTPLCQLSQGIYLTNRNYSISLVTAIAVDVAVRH 120  
QY 121 PLRAGRLSPQAAACAVLVWLVGSLVARWLLGIQEGGFCFRSTRNFMSPRLG 180  
DB 121 PLRAGRLSPQAAACAVLVWLVGSLVARWLLGIQEGGFCFRSTRNFMSPRLG 180  
QY 181 YLPLAVVFCSLKVVYVTAQAORPPTDVQAEATRKAKRWANLLVFWVCFLPLHVLTVR 240  
DB 181 YLPLAVVFCSLKVVYVTAQAORPPTDVQAEATRKAKRWANLLVFWVCFLPLHVLTVR 240  
QY 241 LAVGNACALLETTIRRALYITSKLSDANCCCLDAICYYYMAKEFQESALAVAPRAKHS 300  
DB 241 LAVGNACALLETTIRRALYITSKLSDANCCCLDAICYYYMAKEFQESALAVAPRAKHS 300  
QY 301 QDSLVCVTLA 309  
DB 301 QDSLVCVTLA 309

RESULT 7  
ADO78094  
ID ADO78094 standard; protein; 309 AA.

XX ADO78094;  
XX 26-AUG-2004 (first entry)  
XX Human GPR35.

XX tumour-associated antigen; TAG; cancer; lung cancer; breast cancer;  
KW prostate cancer; colon cancer; stomach cancer; pancreatic cancer;  
KW ear cancer; nose cancer; throat cancer; kidney cancer; cervical cancer;  
KW melanoma; tumour; human; GPR35.

OS Homo sapiens.  
PN DE10254601-A1.  
XX 03-JUN-2004.  
XX 22-NOV-2002; 2002DE-01054601.  
XX 22-NOV-2002; 2002DE-01054601.  
XX (GANY-) GANYMED PHARM AG.

XX Tuereci O, Sahin U, Koslowski M;  
XX WPI; 2004-421820/40.  
XX N-PSDB; ADO78085.

XX Composition containing inhibitor of expression or activity of specific  
XX tumor-associated antigens, useful for treating cancers, also related  
XX compositions for diagnosis and monitoring.

XX Claim 72; SEQ ID NO 9; 124pp; German.

XX The invention relates to pharmaceutical compositions that comprise an  
XX agent that inhibits the expression or activity of a tumour-associated  
XX antigen (TAG) that is encoded by a nucleic acid. The pharmaceutical  
XX compositions and related compositions, are used for treatment of diseases  
XX associated with (abnormal) expression of TAG, specifically cancer e.g. of  
XX lung, breast, prostate, colon, stomach, pancreas, ear/nose/throat, kidney  
XX or cervix, also melanoma. Compositions containing TAG, or related nucleic  
XX acid, antibodies or host cells, are also useful for diagnosis and  
XX monitoring of tumours. The present sequence represents the amino acid  
XX sequence of a human GPR35.

XX Sequence 309 AA;

Query Match 99.6%; Score 1609; DB 8; Length 309;  
Best Local Similarity 99.7%; Pred. No. 1.2e-167;  
Matches 308; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 MNGTYNTCGSSDLTWPPAIIKLGFYAYLVGLVLLGLLNSLALWVFCRMOQTETRIYMT 60  
DB 1 MNGTYNTCGSSDLTWPPAIIKLGFYAYLVGLVLLGLLNSLALWVFCRMOQTETRIYMT 60  
QY 61 NLAVADLCLLCTLPFVLSLRDSTPLCQLSQGIYLTNRNYSISLVTAIAVDVAVRH 120  
DB 61 NLAVADLCLLCTLPFVLSLRDSTPLCQLSQGIYLTNRNYSISLVTAIAVDVAVRH 120  
QY 121 PLRAGRLSPQAAACAVLVWLVGSLVARWLLGIQEGGFCFRSTRNFMSPRLG 180  
DB 121 PLRAGRLSPQAAACAVLVWLVGSLVARWLLGIQEGGFCFRSTRNFMSPRLG 180  
QY 181 YLPLAVVFCSLKVVYVTAQAORPPTDVQAEATRKAKRWANLLVFWVCFLPLHVLTVR 240  
DB 181 YLPLAVVFCSLKVVYVTAQAORPPTDVQAEATRKAKRWANLLVFWVCFLPLHVLTVR 240  
QY 241 LAVGNACALLETTIRRALYITSKLSDANCCCLDAICYYYMAKEFQESALAVAPRAKHS 300  
DB 241 LAVGNACALLETTIRRALYITSKLSDANCCCLDAICYYYMAKEFQESALAVAPRAKHS 300  
QY 301 QDSLVCVTLA 309

```
Db          301 QDSLCVTLA 309
|||||
RESULT 8
ADV73203
ID ADV73203 standard; protein; 309 AA.
XX
AC ADV73203;
XX
DT 10-MAR-2005 (first entry)
XX
DE Human colon tumor cell upregulated protein SEQ ID NO 44.
XX
KW cancer; neoplasm; cytostatic.
XX
OS Homo sapiens.
XX
PN WO2004110345-A2.
XX
PD 23-DEC-2004.
XX
PF 28-OCT-2003; 2003WO-US034019.
XX
PR 29-OCT-2002; 2002US-0422176P.
XX
PA (PHAA ) PHARMACIA CORP.
XX
PI Bourner MJ, Bu JJ, Head RD, Hippenmeyer PJ, Klein BK;
P1 Mazzarella RA, Staten NR;
XX
XX WPI; 2005-039958/04.
DR N-PSDB; ADV73165.
XX
PT New antibody that immunospecifically binds to p-cadherin, useful in
PT preparing a composition for treating or preventing a cancer-associated
PT disorder.
XX
PS Disclosure; SEQ ID NO 44; 257pp; English.
XX
XX The invention relates to an antibody immunospecifically binds to p-
CC cadherin or its fragment. The antibody is useful in preparing a
CC composition for treating or preventing a cancer-associated disorder. The
CC present sequence represents the amino acid sequence of a protein
CC upregulated in human colon cancer cells.
XX
SQ Sequence 309 AA;
Query Match          99.6%; Score 1609; DB 9; Length 309;
Best Local Similarity 99.7%; Pred. No. 1.2e-167;
Matches 308; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MNGTYNTCGSSDLTWPAPKLGFYAVLGVLLVGLLNSLALWVFCRMOQWTETRIYMT 60
Db 1 MNGTYNTCGSSDLTWPAPKLGFYAVLGVLLVGLLNSLALWVFCRMOQWTETRIYMT 60
QY 61 NLAVADCLLCTLPFVLSLRDTSPTPLCQLSGQIYLTNRYSISLVTAIAVDYVAVRH 120
Db 61 NLAVADCLLCTLPFVLSLRDTSPTPLCQLSGQIYLTNRYSISLVTAIAVDYVAVRH 120
QY 121 PLRARGLRSPQAAACAVLWLVIGSLVARNLIGTQEGGCFRSTRHNFNSMRFPFLGF 180
Db 121 PLRARGLRSPQAAACAVLWLVIGSLVARNLIGTQEGGCFRSTRHNFNSMRFPFLGF 180
QY 181 YLPLAVVVFCSLKVVTALAQRPDVGQAEATKAKRWYMANLLVFWCVFLPHVGLTVR 240
Db 181 YLPLAVVVFCSLKVVTALAQRPDVGQAEATKAKRWYMANLLVFWCVFLPHVGLTVR 240
QY 241 LAVGNACALLETIRRALYITSKLSDANCLDAICYNNMAKSFQEASALAVAPRAKAHKS 300
Db 241 LAVGNACALLETIRRALYITSKLSDANCLDAICYNNMAKSFQEASALAVAPRAKAHKS 300
QY 301 QDSLCVTLA 309
|||||
Db          301 QDSLCVTLA 309
|||||
RESULT 9
AEB15039
ID AEB15039 standard; protein; 309 AA.
XX
AC AEB15039;
XX
DT 08-SEP-2005 (first entry)
XX
DE Human GPR35 polypeptide.
XX
KW G-protein coupled receptor 35; GPR35; G-protein coupled receptor; GPCR;
KW screening; cardiovascular disease; gastrointestinal disease;
KW liver disease; cancer; neoplasm; metabolic disorder;
KW hematological disease; respiratory disease; inflammation;
KW neurological disease; urological disorder; cardiovascular-gen.;
KW gastrointestinal-gen.; hepatotropic; cytostatic; metabolic; antianemic;
KW respiratory-gen.; antiinflammatory; neuroprotective; uropathic; receptor.
XX
OS Homo sapiens.
XX
PN WO2005059546-A2.
XX
PD 30-JUN-2005.
XX
PF 02-DEC-2004; 2004WO-EP013679.
PR 12-DEC-2003; 2003EP-00028614.
XX
PA (FARB ) BAYER HEALTHCARE AG.
XX
PI Golz S, Brueggemeier U, Geerts A, Summer H;
XX
XX WPI; 2005-506223/51.
DR N-PSDB; AEB15038.
XX
PT Screening of therapeutic agents useful in treating specified diseases
PT involves contacting test compound with G-protein coupled receptor GPR35,
PT and detect binding of test compound to polypeptide.
XX
PS Disclosure; SEQ ID NO 2; 96pp; English.
XX
XX The invention relates to the use of human G-protein coupled receptor 35
CC (GPR35) for screening therapeutic agents useful in the treatment of
CC cardiovascular disorders, liver and gastrointestinal diseases, cancer
CC disorders, inflammatory diseases, metabolic diseases, hematological
CC disorders, respiratory diseases, neurological disorders and urological
CC disorders, in a mammal. GPR35 is a G-protein coupled receptor (GPCR). The
CC therapeutic agents are screened by contacting a test compound with GPR35
CC polypeptide, and detecting the binding of the test compound to the
CC polypeptide. Also described are: (1) a method of diagnosing the above
CC specified diseases in a mammal, comprising determining the amount of a
CC GPR35 polynucleotide in a sample taken from the mammal, and determining
CC the amount of the GPR35 polynucleotide in healthy and/or diseased mammals
CC; (2) a pharmaceutical composition for treating the above specified
CC diseases in the mammal, comprising a therapeutic agent that binds to the
CC GPR35 polypeptide; (3) use of regulators of a GPR35 for the preparation
CC of the pharmaceutical composition or for the regulation of GPR35 activity
CC in a mammal having the above specified diseases; and (4) a method for the
CC preparation of the pharmaceutical composition, comprising identifying the
CC GPR35 regulator, determining whether the regulator ameliorates the
CC symptoms of the above specified diseases in a mammal, and combining the
CC regulator with an acceptable pharmaceutical carrier. GPR35 is useful for
CC screening therapeutic agents for treating cardiovascular disorders, liver
CC and gastrointestinal diseases, cancer disorders, inflammatory diseases,
CC metabolic diseases, hematological disorders, respiratory diseases,
CC neurological disorders and urological disorders in a mammal, e.g. humans
CC (preferably), dogs, cats, cows, horses, rabbits, and monkeys. This
CC sequence represents human GPR35.
```

```
SQ Sequence 309 AA;
Query Match 99.6%; Score 1609; DB 9; Length 309;
Best Local Similarity 99.7%; Pred. No. 1.2e-167;
Matches 308; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNGYNTCGSSDLTWPPAIIKLGFAVYLVGLVLLVGLLNSLALWVFCRMOQWTEIRYMT 60
DB 1 MNGYNTCGSSDLTWPPAIIKLGFAVYLVGLVLLVGLLNSLALWVFCRMOQWTEIRYMT 60

QY 61 NLAVADLCLLCTLPFVLSLSDTSDTPLCQLSQGIYLTNRNYSISLVTAIADRYAVRH 120
DB 61 NLAVADLCLLCTLPFVLSLSDTSDTPLCQLSQGIYLTNRNYSISLVTAIADRYAVRH 120

QY 121 PLRARGLSRPRQAAVCAVAVLVIGSLVAVRWLGIQEGGFCFSTRNFSMFPPLG 180
DB 121 PLRARGLSRPRQAAVCAVAVLVIGSLVAVRWLGIQEGGFCFSTRNFSMFPPLG 180

QY 181 YLPLAVVVFCSLKVVTALAQRPTDVGQAEATRKARVMWANLLVVFVCFPLHVGLTVR 240
DB 181 YLPLAVVVFCSLKVVTALAQRPTDVGQAEATRKARVMWANLLVVFVCFPLHVGLTVR 240

QY 241 LAVGNACALLETIRRALYITSKLSDANCCCLDAICYYYMAKEFOEASALAVAPRAKAHS 300
DB 241 LAVGNACALLETIRRALYITSKLSDANCCCLDAICYYYMAKEFOEASALAVAPRAKAHS 300

QY 301 QDSLVCVTILA 309
DB 301 QDSLVCVTILA 309

RESULT 10
AAV69989
ID AAV69989 standard; protein; 309 AA.
XX
AC AAV69989;
XX
DT 31-MAY-2000 (first entry)
XX
DE Human receptor-associated protein from Incyte clone 3083742.
XX
KW Human receptor-associated protein; HRAP; Incyte clone 3083742;
KW cystostatic; immunomodulatory; antiinflammatory; cardiast; antianaemic;
KW antiarteriosclerotic; hepatotropic; antiarthritic antirheumatic;
KW antiasthmatic; osteopathic; antiallergic; antidiabetic; dermatological;
KW neuroprotective; diagnosis; treatment; prevention; reproductive disorder;
KW cardiovascular; cell proliferative; autoimmune; inflammatory; allergy;
KW gastrointestinal; atherosclerosis; cirrhosis; leukaemia; cancer; AIDS;
KW arthritis; anaemia; asthma; dermatitis; diabetes; osteoporosis;
KW multiple sclerosis; irritable bowel syndrome.
XX
OS Homo sapiens.
XX
FH Key 2 Location/Qualifiers
FT Modified-site 2 /note= "Potential N-glycosylation site"
FT Modified-site 79 /note= "Potential phosphorylation site"
FT Modified-site 98 /note= "Potential phosphorylation site"
FT Region 102..118 /note= "Potential phosphorylation site"
FT /label= Signature_sequence /note= "G-protein coupled receptor"
FT Modified-site 129 /note= "Potential phosphorylation site"
FT Modified-site 165 /note= "Potential phosphorylation site"
FT Modified-site 191 /note= "Potential phosphorylation site"
FT Modified-site 212 /note= "Potential phosphorylation site"
FT Modified-site 238 /note= "Potential phosphorylation site"
FT Modified-site 238 /note= "Potential phosphorylation site"

FT SQ Sequence 309 AA;
Modified-site 253
/note= "Potential phosphorylation site"
FT Modified-site 261
/note= "Potential phosphorylation site"
FT
FN WO200008155-A2.
XX
XX 17-FEB-2000.
XX
XX 06-AUG-1999; 99WO-US017777.
XX
XX 07-AUG-1998; 98US-0160065P.
XX 01-SEP-1998; 98US-0098703P.
XX (INCY-) INCYTE PHARM INC.
XX Hillman JL, Yue H, Lal P, Tang YT, Gorgone GA, Guegler KJ;
XX Corley NC, Baughn MR;
XX WPI; 2000-205710/18.
XX N-PSDB; AAZ50891.
XX
XX New human receptor-associated proteins (HRAP) useful for the diagnosis,
XX treatment and prevention of cell proliferative, autoimmune, inflammatory,
XX reproductive, cardiovascular, and gastrointestinal disorders.
XX
XX Claim 1; Page 76; 99pp; English.
XX
XX The present sequence is human receptor-associated protein (HRAP) from
XX Incyte clone 3083742 obtained from OVARUN01 cDNA library. This sequence
XX is expressed in haematopoietic/immune, gastrointestinal and reproductive
XX tissues. HRAP has cytostatic, immunomodulatory, antiinflammatory,
XX cardiant, antiarteriosclerotic, hepatotropic, antiarthritic,
XX antirheumatic, osteopathic, antiallergic, antianaemic, antiasthmatic,
XX antidiabetic, dermatological and neuroprotective activities. The present
XX sequence is useful in the diagnosis, treatment and prevention of
XX disorders associated with HRAP expression, especially cell proliferative,
XX autoimmune/inflammatory, reproductive, cardiovascular and
XX gastrointestinal disorders (e.g. atherosclerosis, cirrhosis, leukaemia,
XX cancer, AIDS, arthritis, allergies, anaemia, asthma, dermatitis,
XX diabetes, osteoporosis, multiple sclerosis and irritable bowel syndrome)
XX
XX Sequence 309 AA;
Query Match 99.3%; Score 1603; DB 3; Length 309;
Best Local Similarity 99.4%; Pred. No. 5.4e-167;
Matches 307; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MNGYNTCGSSDLTWPPAIIKLGFAVYLVGLVLLVGLLNSLALWVFCRMOQWTEIRYMT 60
DB 1 MNGYNTCGSSDLTWPPAIIKLGFAVYLVGLVLLVGLLNSLALWVFCRMOQWTEIRYMT 60

QY 61 NLAVADLCLLCTLPFVLSLSDTSDTPLCQLSQGIYLTNRNYSISLVTAIADRYAVRH 120
DB 61 NLAVADLCLLCTLPFVLSLSDTSDTPLCQLSQGIYLTNRNYSISLVTAIADRYAVRH 120

QY 121 PLRARGLSRPRQAAVCAVAVLVIGSLVAVRWLGIQEGGFCFSTRNFSMFPPLG 180
DB 121 PLRARGLSRPRQAAVCAVAVLVIGSLVAVRWLGIQEGGFCFSTRNFSMFPPLG 180

QY 181 YLPLAVVVFCSLKVVTALAQRPTDVGQAEATRKARVMWANLLVVFVCFPLHVGLTVR 240
DB 181 YLPLAVVVFCSLKVVTALAQRPTDVGQAEATRKARVMWANLLVVFVCFPLHVGLTVR 240

QY 241 LAVGNACALLETIRRALYITSKLSDANCCCLDAICYYYMAKEFOEASALAVAPRAKAHS 300
DB 241 LAVGNACALLETIRRALYITSKLSDANCCCLDAICYYYMAKEFOEASALAVAPRAKAHS 300

QY 301 QDSLVCVTILA 309
DB 301 QDSLVCVTILA 309
```





Db 1 MNGTYNTCGSSDLTWPAPKLGFAVYGLVLLVGLLNSLALWVFCRMOQWTETRIYMT 60  
QY 61 NLAVADICLLCTLPFVLHSLRDTSDTPLCQLSQGIYLTNRYMSISLVTAIVDRYAVRH 120  
Db 61 NLAVADICLLCTLPFVLHSLRDTSDTPLCQLSQGIYLTNRYMSISLVTAIVDRYAVRH 120  
QY 121 PLRARGLSRQAAAVCAVWLWVIGSLVARWLLGIOEGGFCFRSTRHNFSMRFPPLG 180  
Db 121 PLRARGLSRQAAAVCAVWLWVIGSLVARWLLGIOEGGFCFRSTRHNFSMRFPPLG 180  
QY 181 YLPLAVVVFCSLKVVTALAQRPTDVQQAETRAKRMWVANLLVFFVCFPLHVGTLVR 240  
Db 181 YLPLAVVVFCSLKVVTALAQRPTDVQQAETRAKRMWVANLLVFFVCFPLHVGTLVR 240  
QY 241 LAVGWNA CALLETIRRALYITSKLSDANCCCLDAICYYYMAKEFOEASALAVAPRAK 300  
Db 241 LAVGWNA CALLETIRRALYITSKLSDANCCCLDAICYYYMAKEFOEASALAVAPRAK 300  
QY 301 QDSLVCVTLA 309  
Db 301 QDSLVCVTLA 309

RESULT 14  
AAV58645  
ID AAY58645 standard; protein; 309 AA.  
XX  
AC AAY58645;  
XX  
DT 11-APR-2000 (first entry)  
XX  
DE Human G-protein coupled receptor GPR35A.  
XX  
KW GPR35A; human; G-protein coupled receptor; purinergic;  
KW 7-transmembrane receptor; antibiotic; antifungal; antiviral; analgesic;  
KW cytosolic; antidiabetic; anorectic; antiaesthetic; antiparkinsonian;  
KW hypotensive; hypertensive; osteopathic; antiangiinal; cardiant;  
KW cerebroprotective; antitumor; antiallergic; antimigraine; antiemetic;  
KW tranquilizer; antidepressant; neuroleptic; nootropic; anticonvulsant;  
KW therapy; diagnosis; vaccine.  
XX  
OS Homo sapiens.  
XX  
FN WO9964452-A1.  
XX  
PD 16-DEC-1999.  
XX  
PF 01-JUN-1999; 95WO-US012123.  
XX  
PR 11-JUN-1998; 98US-00096031.  
XX  
PA (SMIK ) SMITHKLINE BEECHAM CORP.  
XX  
PI Elshourbagy NA;  
XX  
DR WPI; 2000-116525/10.  
DR N-PSDB; AAZ35390.  
XX  
PT New human GPR35A polypeptides and polynucleotides used to identify  
PT agonists, antagonists and inhibitors for use in therapy.  
XX  
FS Claim 1; Page 32-33; 38pp; English.  
XX  
CC The present sequence represents human GPR35A, a novel member of the  
CC purinergic family of polypeptides and a G-protein coupled receptor. The  
CC invention provides GPR35A polypeptides having at least 70% identity with  
CC the present sequence, GPR35A polynucleotides, recombinant materials, and  
CC methods for their production. GPR35A polypeptides can be used for  
CC identifying agonists and antagonists/inhibitors, and for detecting  
CC diseases associated with inappropriate GPR35A activity or levels. GPR35A  
CC polypeptides and polynucleotides, agonists, antagonists and antibodies  
CC are used to treat infections such as bacterial, fungal, protozoan and  
CC viral infections, particularly HIV-1 and HIV-2; pain; cancer; diabetes;

CC obesity; anorexia; bulimia; asthma; Parkinson's disease; acute heart  
CC failure; hypotension; hypertension; urinary retention; osteoporosis;  
CC angina pectoris; myocardial infarction; stroke; ulcers; allergy; benign  
CC prostatic hypertrophy; migraine; vomiting; psychotic and neurological  
CC disorders including anxiety, schizophrenia, manic depression, depression,  
CC delirium, dementia and severe mental retardation; and dyskinesias such as  
CC Huntington's or Gilles de la Tourette's syndrome. The polypeptide is also  
CC useful for production of vaccines  
XX  
SQ Sequence 309 AA;  
Query Match 98.9%; Score 1597; DB 3; Length 309;  
Best Local Similarity 99.0%; Pred. No. 2.5e-166;  
Matches 306; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 MNGTYNTCGSSDLTWPAPKLGFAVYGLVLLVGLLNSLALWVFCRMOQWTETRIYMT 60  
Db 1 MNGTYNTCGSSDLTWPAPKLGFAVYGLVLLVGLLNSLALWVFCRMOQWTETRIYMT 60  
QY 61 NLAVADICLLCTLPFVLHSLRDTSDTPLCQLSQGIYLTNRYMSISLVTAIVDRYAVRH 120  
Db 61 NLAVADICLLCTLPFVLHSLRDTSDTPLCQLSQGIYLTNRYMSISLVTAIVDRYAVRH 120  
QY 121 PLRARGLSRQAAAVCAVWLWVIGSLVARWLLGIOEGGFCFRSTRHNFSMRFPPLG 180  
Db 121 PLRARGLSRQAAAVCAVWLWVIGSLVARWLLGIOEGGFCFRSTRHNFSMRFPPLG 180  
QY 181 YLPLAVVVFCSLKVVTALAQRPTDVQQAETRAKRMWVANLLVFFVCFPLHVGTLVR 240  
Db 181 YLPLAVVVFCSLKVVTALAQRPTDVQQAETRAKRMWVANLLVFFVCFPLHVGTLVR 240  
QY 241 LAVGWNA CALLETIRRALYITSKLSDANCCCLDAICYYYMAKEFOEASALAVAPRAK 300  
Db 241 LAVGWNA CALLETIRRALYITSKLSDANCCCLDAICYYYMAKEFOEASALAVAPRAK 300  
QY 301 QDSLVCVTLA 309  
Db 301 QDSLVCVTLA 309

RESULT 14  
ADA84069  
ID ADA84069 standard; protein; 309 AA.  
XX  
AC ADA84069;  
XX  
DT 20-NOV-2003 (first entry)  
XX  
DE Human GPR35 protein.  
XX  
KW human; marker; expressed sequence tag; EST; arabidopsis; tumour;  
KW stress-induced phenotype; hyperosmotic stress; colon cancer; immunogen;  
KW vaccine.  
XX  
OS Homo sapiens.  
XX  
FN WO2002103028-A2.  
XX  
PD 27-DEC-2002.  
XX  
PF 30-MAY-2002; 2002WO-IB004189.  
XX  
PR 30-MAY-2001; 2001US-0293999P.  
PR 22-OCT-2001; 2001US-0330457P.  
PR 19-FEB-2002; 2002US-0357144P.  
XX  
PA (BIOM-) BIOMEDICAL CENT.  
XX  
PI Baranova AV, Yankovsky NK, Kozlov AP, Lobashev AV, Krukovskaya LL;  
XX WPI; 2003-175241/17.  
XX DR N-PSDB; ADA84068.  
XX

PT Determining if a nucleic acid is a marker for a phenotype/cell type of  
PT interest, by global comparison of expressed sequence tags known to be  
PT expressed in the phenotype/cell type with all ESTs expressed in normal  
PT tissue.

XX Claim 29; Page 448-449; 516pp; English.

XX The invention relates to a novel method for determining if a nucleic acid  
XX is a marker for a predetermined phenotype/cell type of interest from a  
XX biological species. The method comprises performing a global comparison  
XX of a group of expressed sequence tags (ESTs) known to be expressed in the  
XX phenotype/cell type of interest with all ESTs expressed in normal tissue  
XX in order to identify ESTs that are preferentially expressed in the  
XX phenotype/cell of interest. A method of the invention is useful for  
XX determining whether a nucleic acid is a marker for a predetermined  
XX phenotype or cell type of interest from a biological species, preferably  
XX Arabidopsis or human. The cell type of interest is an abnormal cell such  
XX as a tumour cell, and the predetermined phenotype is a stress-induced  
XX phenotype such as hyperosmotic stress or high salt conditions. A method  
XX of the invention is also useful for determining the progression of colon  
XX cancer in a human, for detecting a tumour cell, and for regulating or  
XX preventing the growth of a tumour cell. An antibody of the invention is  
XX useful for detecting the absence or presence of peptides encoded by  
XX tumour-associated markers. A polypeptide of the invention is useful as an  
XX immunogen for vaccinating an animal. The present sequence represents a  
XX tumour-associated antigen of the invention.

XX Sequence 309 AA;

Query Match 98.9%; Score 1597; DB 6; Length 309;  
Best Local Similarity 99.0%; Pred. No. 2.5e-166;  
Matches 306; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MNGTYNTCGSSDLTWPPAIKLGFYAYLVGLVLLVGLLNSLALWVFCRMOQWTTETRIYMT 60  
DB |||||||  
QY 1 MNGTYNTCGSSDLTWPPAIKLGFYAYLVGLVLLVGLLNSLALWVFCRMOQWTTETRIYMT 60  
DB |||||||  
QY 61 NLAVADLCCLCTLPFVLSLSDTSDTPLCQLSQGIYLTNRYSISLVTAIAVDRIYVAVRH 120  
DB |||||||  
QY 61 NLAVADLCCLCTLPFVLSLSDTSDTPLCQLSQGIYLTNRYSISLVTAIAVDRIYVAVRH 120  
DB |||||||  
QY 121 PLRARGLRSPROAAACAVLWLVIGSLVARWLLGIQEGGFCFRSTRHNFNSMRPPLIGF 180  
DB |||||||  
QY 121 PLRARGLRSPROAAACAVLWLVIGSLVARWLLGIQEGGFCFRSTRHNFNSMRPPLIGF 180  
DB |||||||  
QY 181 YLPLAVVVFCSLKVVTALAQRPTDVQQAETRKAKRMVWVANLLVFVVCFLPLHVLGLTVR 240  
DB |||||||  
QY 181 YLPLAVVVFCSLKVVTALAQRPTDVQQAETRKAKRMVWVANLLVFVVCFLPLHVLGLTVR 240  
DB |||||||  
QY 241 LAVGNWACALLETIRRALYITSKLSDANCCLDIAICYNNMAKFBQASALAVAPRAKAKHS 300  
DB |||||||  
QY 241 LAVGNWACALLETIRRALYITSKLSDANCCLDIAICYNNMAKFBQASALAVAPRAKAKHS 300  
DB |||||||  
QY 301 QDSLVCVTILA 309  
DB |||||||  
QY 301 QDSLVCVTILA 309  
DB |||||||

RESULT 15

AD078095  
ID AD078095 standard; protein; 394 AA.

XX AC AD078095;

XX 26-AUG-2004 (first entry)

XX Human GPR35 isoform.

XX tumour-associated antigen; Tag; cancer; lung cancer; breast cancer;  
KW prostate cancer; colon cancer; stomach cancer; pancreatic cancer;  
KW ear cancer; nose cancer; throat cancer; kidney cancer; cervical cancer;  
KW melanoma; tumour; human; GPR35.

OS Homo sapiens.  
XX DE10254601-A1.  
XX 03-JUN-2004.

XX 22-NOV-2002; 2002DE-01054601.

XX 22-NOV-2002; 2002DE-01054601.

XX (GANY-) GANYMED PHARM AG.

XX Tueci O, Sahin U, Koslowski M;

XX WPI; 2004-421820/40.

XX Composition containing inhibitor of expression or activity of specific  
XX tumor-associated antigens, useful for treating cancers, also related  
XX compositions for diagnosis and monitoring.

XX Claim 72; SEQ ID NO 10; 124pp; German.

XX The invention relates to pharmaceutical compositions that comprise an  
XX agent that inhibits the expression or activity of a tumour-associated  
XX antigen (Tag) that is encoded by a nucleic acid. The pharmaceutical  
XX compositions and related compositions, are used for treatment of diseases  
XX associated with (abnormal) expression of Tag, specifically cancer e.g. of  
XX lung, breast, prostate, colon, stomach, pancreas, ear/nose/throat, kidney  
XX or cervix, also melanoma. Compositions containing Tag, or related nucleic  
XX acid, antibodies or host cells, are also useful for diagnosis and  
XX monitoring of tumours. The present sequence represents the amino acid  
XX sequence of a human GPR35.

XX Sequence 394 AA;

Query Match 98.9%; Score 1597; DB 8; Length 394;  
Best Local Similarity 99.0%; Pred. No. 3.3e-166;  
Matches 306; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MNGTYNTCGSSDLTWPPAIKLGFYAYLVGLVLLVGLLNSLALWVFCRMOQWTTETRIYMT 60  
DB |||||||  
QY 86 MNGTYNTCGSSDLTWPPAIKLGFYAYLVGLVLLVGLLNSLALWVFCRMOQWTTETRIYMT 145  
DB |||||||  
QY 61 NLAVADLCCLCTLPFVLSLSDTSDTPLCQLSQGIYLTNRYSISLVTAIAVDRIYVAVRH 120  
DB |||||||  
QY 146 NLAVADLCCLCTLPFVLSLSDTSDTPLCQLSQGIYLTNRYSISLVTAIAVDRIYVAVRH 205  
DB |||||||  
QY 121 PLRARGLRSPROAAACAVLWLVIGSLVARWLLGIQEGGFCFRSTRHNFNSMRPPLIGF 180  
DB |||||||  
QY 206 PLRARGLRSPROAAACAVLWLVIGSLVARWLLGIQEGGFCFRSTRHNFNSMRPPLIGF 265  
DB |||||||  
QY 181 YLPLAVVVFCSLKVVTALAQRPTDVQQAETRKAKRMVWVANLLVFVVCFLPLHVLGLTVR 240  
DB |||||||  
QY 266 YLPLAVVVFCSLKVVTALAQRPTDVQQAETRKAKRMVWVANLLVFVVCFLPLHVLGLTVR 325  
DB |||||||  
QY 241 LAVGNWACALLETIRRALYITSKLSDANCCLDIAICYNNMAKFBQASALAVAPRAKAKHS 300  
DB |||||||  
QY 326 LAVGNWACALLETIRRALYITSKLSDANCCLDIAICYNNMAKFBQASALAVAPRAKAKHS 385  
DB |||||||  
QY 301 QDSLVCVTILA 309  
DB |||||||  
QY 386 QDSLVCVTILA 394  
DB |||||||

Search completed: February 9, 2006, 00:54:43  
Job time : 215.5 secs

GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: February 9, 2006, 01:00:39 : Search time 33.5 Seconds  
(without alignments)  
762.591 Million cell updates/sec

Title: US-10-083-168-16

Perfect score: 1614

Sequence: 1 MNGYNTCGSSDLTPPAIK.....AVAPRAKHSQDSLCTVLA 309

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*

- 1: /cgn2\_6/ptodata/1/iaa/5 COMB.pap:\*
- 2: /cgn2\_6/ptodata/1/iaa/6 COMB.pap:\*
- 3: /cgn2\_6/ptodata/1/iaa/H COMB.pap:\*
- 4: /cgn2\_6/ptodata/1/iaa/PCTUS COMB.pap:\*
- 5: /cgn2\_6/ptodata/1/iaa/RE COMB.pap:\*
- 6: /cgn2\_6/ptodata/1/iaa/backfiles1.pap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description        |
|------------|-------|-------------|--------|----|--------------------|
| 1          | 1614  | 100.0       | 309    | 2  | US-09-422-869-20   |
| 2          | 402   | 24.9        | 370    | 2  | US-08-781-250-2    |
| 3          | 381.5 | 23.6        | 363    | 2  | US-10-314-048A-159 |
| 4          | 375.5 | 23.3        | 367    | 2  | US-10-314-048A-36  |
| 5          | 368.5 | 22.8        | 387    | 2  | US-09-170-496D-108 |
| 6          | 368.5 | 22.8        | 387    | 2  | US-09-170-496D-222 |
| 7          | 368.5 | 22.8        | 387    | 2  | US-09-944-807-21   |
| 8          | 368.5 | 22.8        | 387    | 2  | US-10-314-048A-135 |
| 9          | 362   | 22.4        | 372    | 2  | US-09-875-076-4    |
| 10         | 361.5 | 22.4        | 344    | 1  | US-08-467-948A-8   |
| 11         | 361.5 | 22.4        | 344    | 2  | US-08-467-947A-8   |
| 12         | 360.5 | 22.3        | 302    | 1  | US-08-467-948A-30  |
| 13         | 360.5 | 22.3        | 302    | 2  | US-08-467-947A-30  |
| 14         | 348.5 | 21.6        | 360    | 2  | US-10-314-048A-137 |
| 15         | 341.5 | 21.2        | 351    | 2  | US-10-314-048A-157 |
| 16         | 341   | 21.1        | 361    | 2  | US-10-314-048A-139 |
| 17         | 334.5 | 20.7        | 254    | 2  | US-09-964-956-83   |
| 18         | 330.5 | 20.5        | 377    | 2  | US-09-745-842-17   |
| 19         | 329.5 | 20.4        | 374    | 2  | US-09-102-710B-3   |
| 20         | 327   | 20.3        | 346    | 2  | US-10-314-048A-24  |
| 21         | 322.5 | 20.0        | 345    | 2  | US-09-979-603-18   |
| 22         | 321   | 19.9        | 362    | 2  | US-08-513-974B-374 |
| 23         | 320.5 | 19.9        | 343    | 2  | US-10-314-048A-151 |
| 24         | 319.5 | 19.8        | 346    | 2  | US-09-585-876-2    |
| 25         | 318   | 19.7        | 374    | 2  | US-09-745-842-15   |
| 26         | 317.5 | 19.7        | 346    | 2  | US-09-979-603-2    |
| 27         | 317.5 | 19.7        | 346    | 2  | US-10-314-048A-14  |

|    |       |      |     |   |                    |                   |
|----|-------|------|-----|---|--------------------|-------------------|
| 28 | 317.5 | 19.7 | 346 | 2 | US-10-314-048A-88  | Sequence 88, Appl |
| 29 | 317   | 19.6 | 309 | 2 | US-09-979-603-22   | Sequence 22, Appl |
| 30 | 317   | 19.6 | 373 | 2 | US-08-513-974B-373 | Sequence 373, App |
| 31 | 315.5 | 19.5 | 365 | 2 | US-09-745-842-16   | Sequence 16, Appl |
| 32 | 315.5 | 19.5 | 365 | 2 | US-09-077-173D-2   | Sequence 2, Appl  |
| 33 | 312.5 | 19.4 | 364 | 2 | US-08-148-708-2    | Sequence 2, Appl  |
| 34 | 311.5 | 19.3 | 391 | 2 | US-09-826-509-463  | Sequence 463, App |
| 35 | 310.5 | 19.2 | 327 | 2 | US-08-513-974B-372 | Sequence 372, App |
| 36 | 310.5 | 19.2 | 362 | 2 | US-09-170-496D-166 | Sequence 166, App |
| 37 | 310   | 19.2 | 342 | 2 | US-08-988-876-9    | Sequence 9, Appl  |
| 38 | 308.5 | 19.1 | 375 | 1 | US-08-442-134A-2   | Sequence 2, Appl  |
| 39 | 308.5 | 19.1 | 375 | 1 | US-08-444-581B-2   | Sequence 2, Appl  |
| 40 | 308.5 | 19.1 | 375 | 1 | US-08-446-088A-2   | Sequence 2, Appl  |
| 41 | 308.5 | 19.1 | 375 | 1 | US-08-559-524A-3   | Sequence 3, Appl  |
| 42 | 308.5 | 19.1 | 375 | 2 | US-08-749-707-3    | Sequence 3, Appl  |
| 43 | 308.5 | 19.1 | 375 | 2 | US-09-947-922-3    | Sequence 3, Appl  |
| 44 | 306   | 19.0 | 328 | 2 | US-08-513-974B-39  | Sequence 39, Appl |
| 45 | 306   | 19.0 | 328 | 2 | US-08-513-974B-371 | Sequence 371, App |

#### ALIGNMENTS

##### RESULT 1

US-09-422-869-20

; Sequence 20, Application US/09422869

; Patent No. 6235481

; GENERAL INFORMATION:

; APPLICANT: POLONSKY, KENNETH S.

; APPLICANT: HORIKAWA, YUKIO

; APPLICANT: ODA, NAOHISA

; APPLICANT: COX, NANCY J.

; APPLICANT: SREENAN, SEAMUS

; APPLICANT: ZHOU, YUN-PING

; APPLICANT: OTANI, KENICHI

; APPLICANT: HANIS, CRAIG L.

; APPLICANT: BELL, GRAEME I.

; TITLE OF INVENTION: METHODS OF TREATMENT OF TYPE 2 DIABETES

; FILE REFERENCE: ARCD:307

; CURRENT APPLICATION NUMBER: US/09/422,869

; CURRENT FILING DATE: 1999-10-21

; EARLIER APPLICATION NUMBER: 60/134,175

; EARLIER FILING DATE: 1999-05-13

; NUMBER OF SEQ ID NOS: 30

; SOFTWARE: Patent in Ver. 2.0

; SEQ ID NO 20

; LENGTH: 309

; TYPE: PRT

; ORGANISM: Human

US-09-422-869-20

Query Match 100.0%; Score 1614; DB 2; Length 309;

Best Local Similarity 100.0%; Pred. No. 1.1e-129;

Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

|    |     |   |     |
|----|-----|---|-----|
| QY | 1   | MNGYNTCGSSDLTPPAIKLGFAYLGLVLLGLLNSLALWVFCRMOQTETRIYMT     | 60  |
| DB | 1   | MNGYNTCGSSDLTPPAIKLGFAYLGLVLLGLLNSLALWVFCRMOQTETRIYMT     | 60  |
| QY | 61  | NLAVALDCLLCTLPFLVHSLRDTSTPLCOLSQGIYLTNRNYSISLVTAIADRVAVRH | 120 |
| DB | 61  | NLAVALDCLLCTLPFLVHSLRDTSTPLCOLSQGIYLTNRNYSISLVTAIADRVAVRH | 120 |
| QY | 121 | PLRAGRLSPQAAACAVLWLVIGSLVARWLGIQGGFCFSTRHNFNMRPPLGFG      | 180 |
| DB | 121 | PLRAGRLSPQAAACAVLWLVIGSLVARWLGIQGGFCFSTRHNFNMRPPLGFG      | 180 |
| QY | 181 | YLPLAVVFCSLKVVYALAQRPPTDVQAEATRKAAVMWNLIVFVVCFLPLHVLTVR   | 240 |
| DB | 181 | YLPLAVVFCSLKVVYALAQRPPTDVQAEATRKAAVMWNLIVFVVCFLPLHVLTVR   | 240 |
| QY | 241 | LAVGNACALLETIRALYITSKLSDANCCLDIAICVYTMKEFOFASALAVAPRAKHS  | 300 |



Db 267 EVYRSVDLAFFITLSFTYNSMLDPVYVYFSSPSF 301

## RESULT 4

US-10-314-048A-36  
; Sequence 36, Application US/10314048A

; Patent No. 6902902

; GENERAL INFORMATION:

; APPLICANT: Unett, David J.

; APPLICANT: Chen, Ruoping

; APPLICANT: Richman, Jeremy

; APPLICANT: Connolly, Daniel

; APPLICANT: Dang, Huong T.

; APPLICANT: Choi, Bryan

; APPLICANT: Leonard, James

; APPLICANT: Hakak, Yaron

; APPLICANT: Liaw, Chen

; APPLICANT: Lowitz, Kevin P.

; APPLICANT: Behan, Dominic P.

; APPLICANT: Chalmers, Derek T.

; APPLICANT: Lerner, Michael

; TITLE OF INVENTION: Human G Protein-Coupled Receptors and Modulators Thereof

; FILE REFERENCE: For the Treatment of Metabolic-Related Disorders

; CURRENT APPLICATION NUMBER: US/10/314,048A

; CURRENT FILING DATE: 2002-12-06

; PRIOR APPLICATION NUMBER: 10/096,511

; PRIOR FILING DATE: 2002-03-12

; PRIOR APPLICATION NUMBER: 09/995,543

; PRIOR FILING DATE: 2001-11-27

; PRIOR APPLICATION NUMBER: 60/399,917

; PRIOR FILING DATE: 2002-07-29

; PRIOR APPLICATION NUMBER: 60/404,761

; PRIOR FILING DATE: 2002-08-19

; PRIOR APPLICATION NUMBER: 60/410,747

; PRIOR FILING DATE: 2002-09-13

; NUMBER OF SEQ ID NOS: 161

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 36:

; LENGTH: 363

; TYPE: PRP

; ORGANISM: Homo sapiens

US-10-314-048A-36

Query Match 23.3%; Score 375.5; DB 2; Length 363;

Best Local Similarity 34.1%; Pred. No. 2.8e-24;

Matches 94; Conservative 48; Mismatches 107; Indels 27; Gaps 10;

QY 27 LGVLVLGLLNSLALWVFCRCMQOWTETRIYMTNLAVADLCCLCTLPFVLHSL-----R 81

Db 34 LGLEFIFGLLGNGLALWIFCFHLKSKSRIFLFLNLAVADFLIICLPFLMDNYVRRWDW 93

QY 82 DTSPTPLCOLSQGIYLTNRYMSISLVAIAVDYVAVRHPLRARGLSRPRQAAVCAVLW 141

Db 94 KEGDIP-CRLVLFWMNRQSGIIFLTVAVDYVAVRHPLRARGLSRPRQAAVCAVLW 152

QY 142 VLVIGSLV--ARWLGIQGG--FCPR-STRNPF--NSMRPFLGFLPLAVVFCSLKV 194

Db 153 GITIGLTVHLKKGKQIPQNGANLCSFSICHTFQWHEAMF-LLEFFPLGLIILFCSARI 211

QY 195 VTALAQRPTDVGQAEATKAARMWVANLLVFCPLPLHGLTVRLAVGW-----NA 247

Db 212 IWSLRQR---QMDRHAKIKRAITFMVVAIVFVICFLP---SVVVRIRFWLLHSTGTON 265

QY 248 CALLETIRRALYITSKLSANCCDAICYYYMAKEF 283

Db 266 CEVYRSVDLAFFITLSFTYNSMLDPVYVYFSSPSF 301

## RESULT 5

US-09-170-496D-108

; Sequence 108, Application US/09170496D

; Patent No. 6555339

; GENERAL INFORMATION:

; APPLICANT: Behan, Dominic P.

; APPLICANT: Chalmers, Derek T.

; APPLICANT: Liaw, Chen W.

; TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein-

; TITLE OF INVENTION: Receptors

; FILE REFERENCE: AREN-0040

; CURRENT APPLICATION NUMBER: US/09/170,496D

; CURRENT FILING DATE: 1998-10-13

; NUMBER OF SEQ ID NOS: 294

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 108

; LENGTH: 387

; TYPE: PRP

; ORGANISM: Homo sapiens

US-09-170-496D-108

Query Match 22.8%; Score 368.5; DB 2; Length 387;

Best Local Similarity 34.3%; Pred. No. 1.2e-23;

Matches 95; Conservative 48; Mismatches 105; Indels 29; Gaps 11;

QY 27 LGVLVLGLLNSLALWVFCRCMQOWTETRIYMTNLAVADLCCLCTLPFVL-----HSLR 81

Db 34 LGLEFIFGLLGNGLALWIFCFHLKSKSRIFLFLNLAVADFLIICLPFVMDYVRRSDW 93

QY 82 DTSPTPLCOLSQGIYLTNRYMSISLVAIAVDYVAVRHPLRARGLSRPRQAAVCAVLW 141

Db 94 NFGDIP-CRLVLFWMNRQSGIIFLTVAVDYVAVRHPLRARGLSRPRQAAVCAVLW 152

QY 142 VLVIG---SLVARWLLGIQGG--GFCPR-STRNPF--NSMRPFLGFLPLAVVFCSLK 193

Db 153 GITVGLTVHLKKGKLL-IQNGPANVCISFSICHTFRWHEAMF-LLEFFLPLGLIILFCSAR 210

QY 194 VTALAQRPTDVGQAEATKAARMWVANLLVFCPLPLHGLTVRLAVGW-----N 246

Db 211 IWSLRQR---QMDRHAKIKRAITFMVVAIVFVICFLP---SVVVRIRFWLLHSTGTO 264

QY 247 ACALLETIRRALYITSKLSANCCDAICYYYMAKEF 283

Db 265 NCEVYRSVDLAFFITLSFTYNSMLDPVYVYFSSPSF 301

## RESULT 6

US-09-170-496D-222

; Sequence 222, Application US/09170496D

; Patent No. 6555339

; GENERAL INFORMATION:

; APPLICANT: Behan, Dominic P.

; APPLICANT: Chalmers, Derek T.

; APPLICANT: Liaw, Chen W.

; TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein-

; TITLE OF INVENTION: Receptors

; FILE REFERENCE: AREN-0040

; CURRENT APPLICATION NUMBER: US/09/170,496D

; CURRENT FILING DATE: 1998-10-13

; NUMBER OF SEQ ID NOS: 294

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 222

; LENGTH: 387

; TYPE: PRP

; ORGANISM: Homo sapiens

US-09-170-496D-222

Query Match 22.8%; Score 368.5; DB 2; Length 387;

Best Local Similarity 34.1%; Pred. No. 1.2e-23;

Matches 94; Conservative 47; Mismatches 108; Indels 27; Gaps 10;

QY 27 LGVLVLGLLNSLALWVFCRCMQOWTETRIYMTNLAVADLCCLCTLPFVLHSLRDTSDT 86

Db 34 LGLEFIFGLLGNGLALWIFCFHLKSKSRIFLFLNLAVADFLIICLPFVMDYVRRSDW 93

QY 87 PL-----COLSQGIYLTNRYMSISLVAIAVDYVAVRHPLRARGLSRPRQAAVCAVLW 142

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Db 94 KFGDIPCLRLVLPFAMNRQSGIIFLTVAADRYFRVPHHAKNKNWTAATIIISCLLWG 153
QY 143 LVIG---SLVARWLLGIOEG--GFCFR-STRNPF--NSMRPPLGFLYPLAVVVFCSLKV 194
Db 154 ITVGLTVHLLKKLL-IQNGPANVCISFSICHTFRWHEAMF-LLEFLPLGLIILFCSARI 211
QY 195 VTALAQRPTDVGQAEATRAKARMWVANLLVFVCFPLHVLGTLVRLAVGW-----NA 247
Db 212 IWSLRQ---QMDRHAKIKRAITFMVVAIVFVICFLP---SVVVRIRIFWLLHTSGTQ 265
QY 248 ACALLETIRRALYITSKLSANCLDAICYYYMAKEF 283
Db 266 NCEVRSVDLAPFITLSFTYMNMLDPVVYFSSPSF 301

RESULT 7
US-09-944-807-21
; Sequence 21, Application US/09944807
; Patent No. 673895
; GENERAL INFORMATION:
; APPLICANT: Boehringer Ingelheim Pharma KG
; TITLE OF INVENTION: Method for identifying substances which positively
; TITLE OF INVENTION: influence inflammatory conditions of chronic
; TITLE OF INVENTION: inflammatory airway diseases
; FILE REFERENCE: 082.00n
; CURRENT APPLICATION NUMBER: US/09/944,807
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: UK 0021484.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 21
; LENGTH: 387
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-944-807-21

Query Match 22.8%; Score 368.5; DB 2; Length 387;
Best Local Similarity 34.3%; Pred. No. 1.2e-23;
Matches 95; Conservative 48; Mismatches 105; Indels 29; Gaps 11;

QY 27 LGVLLVGLLNSLALWVFCRMOQWETETRIYMTNLAVADCLCLTLPFVL-----HSLR 81
Db 34 LGLEFIFGLLNGLALWIFCFHLKSKSRIFLFLNLAADFLLIICLPFVMDYVYRRSDW 93
QY 82 DTSDFPLCQLSGIYLTNRYMSISLVTAIAVDRYAVRHPRLRARGLSRQAAAVCAVLW 141
Db 94 NFGDIP-CRLVLPFAMNRQSGIIFLTVAADRYFRVPHHAKNKNWTAATIIISCLLW 152
QY 142 VLIVG---SLVARWLLGIOEG--GFCFR-STRNPF--NSMRPPLGFLYPLAVVVFCSLK 193
Db 153 GITVGLTVHLLKKLL-IQNGPANVCISFSICHTFRWHEAMF-LLEFLPLGLIILFCSAR 210
QY 194 VTALAQRPTDVGQAEATRAKARMWVANLLVFVCFPLHVLGTLVRLAVGW-----N 246
Db 211 IWSLRQ---QMDRHAKIKRAITFMVVAIVFVICFLP---SVVVRIRIFWLLHTSGTQ 264
QY 247 ACALLETIRRALYITSKLSANCLDAICYYYMAKEF 283
Db 265 NCEVRSVDLAPFITLSFTYMNMLDPVVYFSSPSF 301

RESULT 8
US-10-314-048A-135
; Sequence 135, Application US/10314048A
; Patent No. 6902902
; GENERAL INFORMATION:
; APPLICANT: Unett, David J.
; APPLICANT: Chen, Ruoping
; APPLICANT: Richman, Jeremy
; APPLICANT: Connolly, Daniel
; APPLICANT: Dang, Huong T.
; APPLICANT: Choi, Bryan

Db 94 KFGDIPCLRLVLPFAMNRQSGIIFLTVAADRYFRVPHHAKNKNWTAATIIISCLLWG 153
QY 143 LVIG---SLVARWLLGIOEG--GFCFR-STRNPF--NSMRPPLGFLYPLAVVVFCSLKV 194
Db 154 ITVGLTVHLLKKLL-IQNGPANVCISFSICHTFRWHEAMF-LLEFLPLGLIILFCSARI 211
QY 195 VTALAQRPTDVGQAEATRAKARMWVANLLVFVCFPLHVLGTLVRLAVGW-----NA 247
Db 212 IWSLRQ---QMDRHAKIKRAITFMVVAIVFVICFLP---SVVVRIRIFWLLHTSGTQ 265
QY 248 ACALLETIRRALYITSKLSANCLDAICYYYMAKEF 283
Db 266 NCEVRSVDLAPFITLSFTYMNMLDPVVYFSSPSF 301

RESULT 9
US-09-875-076-4
; Sequence 4, Application US/09875076
; Patent No. 6869776
; GENERAL INFORMATION:
; APPLICANT: Chen, Ruoping
; APPLICANT: Dang, Huong T.
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors
; FILE REFERENCE: AREN0050
; CURRENT APPLICATION NUMBER: US/09/875,076
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 09/417,044
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 60/120,416
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/121,851
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; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/123,946
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,949
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/136,436
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,437
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,439
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,567
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/137,127
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/137,131
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/141,448
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: 60/156,653
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/156,633
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/156,555
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/156,634
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/157,280
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,294
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,281
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,293
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,282
; PRIOR FILING DATE: 1999-10-01
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 4
; LENGTH: 372
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-875-076-4

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Query Match      22.4%; Score 362; DB 2; Length 372;
Best Local Similarity 33.7%; Pred. No. 4e-23;
Matches 109; Conservative 47; Mismatches 125; Indels 42; Gaps 12;

QY 6 NTCGSSDLTWP---PAIKLGFYAYLGVLLVGLLNSLALVFCRCMQQWETRIYMTNL 62
DB 6 SSTSSVLPDYPYRTHRLHVVY-SLVLAAGLPLNALAVFLRALRVHSVVMCNL 64
QY 63 AVADLCCLCTLP-----FVLHSLRDTSDTP-----LCQLSQGIYLTNRVMSISLVAIAVD 113
DB 65 AASDLLFTLSLVRISYALH-----HWPFDDLLCQTTGALFOMMYGSCIFMLINVD 118
QY 114 RVAVVRHPLRARGLRSPQAAVCAVLVVLVIGSLV-----ARWLLGIGEGGFCFRS 165
DB 119 RVAIVHPLRLHRLRPRVARLLCLGWALILVFAVPAARVHRPSCRDRDLEVLRCFES 178
QY 166 -TRHFNNSMRFL-----LGFVPLAVVVFCSLKVVTALAOPTDVGQAEATRKAAKM 218
DB 179 FSELMKGRLLPLVLAALGELLPLAAVYSSGRVFWTLA-RP--DATQSORRRKTVRL 235
QY 219 VVANLLVVFVCPPLHVGITV----RLAVGNACALLETIRRALYITSKLSANCCCLDAI 274
DB 236 LLANLVIFLLCFVPYNSTLAVYGLRSLKLAASVPARDVRGVLMVWLLAGANCVLDPL 295
QY 275 CYTMAKEFOEA-SALAVAPRAK 296
DB 296 VTFFSAGFNRLRGLGTTHRAR 318

```

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RESULT 10
US-08-467-948A-8
; Sequence 8, Application US/08467948A
; Patent No. 5998164
; GENERAL INFORMATION:
; APPLICANT: LI, YI
; APPLICANT: CAO, LIANG
; APPLICANT: NI, JIAN
; APPLICANT: GENTZ, REINER
; APPLICANT: BULT, CAROL J.
; APPLICANT: SUTTON III, GRANGER G.
; APPLICANT: ROSEN, CRAIG A.
; TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein
; TITLE OF INVENTION: Coupled Receptor GPR2
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVE., NW, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467,948A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04079
; FILING DATE: 30-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: STEFFE, ERIC K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.1140003/EKS/KLM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 344 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-467-948A-8

Query Match      22.4%; Score 361.5; DB 1; Length 344;
Best Local Similarity 29.2%; Pred. No. 4e-23;
Matches 90; Conservative 68; Mismatches 107; Indels 43; Gaps 10;

QY 10 SSDLTWPPAIKLGFFAYL-GVLLVGLLNSLALVFCRCMQQWETRIYMTNLAVADLC 68
DB 6 SHCFYNDSFKTLGCMFSVFLGLISNCVAIFICVLKVRNETTYTMINLMSDLL 65
QY 69 LLCTLPFLVHSLRDTSDTP-----LCQLSQGIYLTNRVMSISLVAIAVDYVAVRHPLRA 124
DB 66 FVFTLPFRIFYF-TTRNWPFGDLLCKISVLMFYTNMYSILFLTCISVDRFLAIVVYFPKS 124
QY 125 RGLRSPQAAVCAVLVVLVI-GSLVARWLLGIQEGG-----FCFSTRHNFNSMRF-- 176
DB 125 KTLRTKRNKAVICTGVMLTVIGGSAPAVFVQSTHSGQNNASACFEN-----FPEA 175
QY 177 -----LLGFVPLAVVVFCSLKVVTALAOPTDVGQAEATR-KAARMVWA 221
DB 176 TWKTYLSRIVIFIEIVGFFIFLILNVTCSMWLKLTK--PVTLSRSKINKTKVLKXIFV 233
QY 222 NLLVVFVVCFLPHVGLTVRLAVGNWA---CALLETIRRALYITSKLSANCCCLDAICYYY 278
DB 234 HLIIIFCFVFPYNINILYSLVTRTQTFVNCVVAARVTWYPTILCIAVSNCCFDPVIVYF 293

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[illegible]





QY 292 AP-----RAVAHKSOD-----SLC 305  
Db 306 KPRPGRSQARRESEMPISNLC 327  
Search completed: February 9, 2006, 01:02:27  
Job time : 34.5 secs

Db 210 WSLRQR---QMDRHAKIKRAINFMVVAIVFICFLP---SVAVRIRIFWLLKYKVRNC 263  
QY 249 ALLETIRRALYITSKJSDANCCCLDAICYYYMAKEF 283  
Db 264 DIYSSVDLAFFTLSTFTYMSMLDPVVYYFSPSF 298

## RESULT 15

US-10-314-048A-157  
; Sequence 157, Application US/10314048A  
; Patent No. 6902902  
; GENERAL INFORMATION:  
; APPLICANT: Unsett, David J.  
; APPLICANT: Chen, Ruoping  
; APPLICANT: Richman, Jeremy  
; APPLICANT: Connolly, Daniel  
; APPLICANT: Dang, Huong T.  
; APPLICANT: Choi, Bryan  
; APPLICANT: Leonard, James  
; APPLICANT: Hakak, Yaron  
; APPLICANT: Liaw, Chen  
; APPLICANT: Lowitz, Kevin P.  
; APPLICANT: Behan, Dominic P.  
; APPLICANT: Chalmers, Derek T.  
; APPLICANT: Lerner, Michael  
; TITLE OF INVENTION: Human G Protein-Coupled Receptors and Modulators Thereof  
; FILE REFERENCE: 22.US6.CIP  
; CURRENT APPLICATION NUMBER: US/10/314,048A  
; CURRENT FILING DATE: 2002-12-06  
; PRIOR APPLICATION NUMBER: 10/096,511  
; PRIOR FILING DATE: 2002-03-12  
; PRIOR APPLICATION NUMBER: 09/995,543  
; PRIOR FILING DATE: 2001-11-27  
; PRIOR APPLICATION NUMBER: 60/399,917  
; PRIOR FILING DATE: 2002-07-29  
; PRIOR APPLICATION NUMBER: 60/404,761  
; PRIOR FILING DATE: 2002-08-19  
; PRIOR APPLICATION NUMBER: 60/410,747  
; PRIOR FILING DATE: 2002-09-13  
; NUMBER OF SEQ ID NOS: 161  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 157  
; LENGTH: 351  
; TYPE: PRT  
; ORGANISM: Rat  
US-10-314-048A-157

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Best Local Similarity 33.2%; Pred. No. 2.1e-21;  
Matches 107; Conservative 48; Mismatches 114; Indels 53; Gaps 15;  
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Db 138 RTAAAIVCVLTWLVILGTV--YLL--MESHLCVRGMVSSCESFIMESANGWHDIMFQ-LE 192  
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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 11, 2006, 02:58:32 ; Search time 5114 Seconds  
(without alignments)  
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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues  
Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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10: gb\_sts.\*  
11: gb\_sy.\*  
12: gb\_un.\*  
13: gb\_vi.\*  
14: gb\_hcg.\*  
15: gb\_pl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 4          | 922   | 99.1        | 2270   | AK172786 | Homo sapi   |
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| 28 | 114.4 | 12.3 | 1089   | 11 | BT019417 | Synthetic   |
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ALIGNMENTS

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DEFINITION Sequence 1 from Patent WO2005059546.  
ACCESSION CS122237  
VERSION CS122237.1 GI:70911057  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE 1  
AUTHORS Golz, S.  
TITLE Diagnostics and therapeutics for diseases associated with g  
protein-coupled receptor 35 (gpr35)  
JOURNAL Patent: WO 2005059546-A 1 30-JUN-2005;  
Bayer HealthCare AG (DE)  
FEATURES  
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| ORIGIN | Query Match           | 99.5%  | Score        | 925.2;  | DB         | 6; | Length | 930; |
|        | Best Local Similarity | 99.7%;   | Pred. No.    | 1e-120; |            |    |        |      |
|        | Matches               | 927;   | Conservative | 0;      | Mismatches | 3; | Indels | 0;   |
|        | Gaps                  | 0  |              |         |            |    |        |      |
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| Qy     | 61                    | CTGGGCTTCTACGCCTACTTGGGCGTCTGTGTGTCTAGGCTGTCTCAACAGCCTG    | 120          |         |            |    |        |      |
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| Qy     | 121                   | GGCTCTGGGGTTCTGTCTGCCGATGCGAGTGGACGGAGACCCGGATCTACATGACC   | 180          |         |            |    |        |      |
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LOCUS
DEFINITION    Homo sapiens G protein-coupled receptor (GPR35) gene, complete cds.
ACCESSION     AF027957
VERSION       AF027957.1 GI:2739108
KEYWORDS
SOURCE        Homo sapiens (human)
ORGANISM      Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
              Homnidae; Homo.
REFERENCE     1 (bases 1 to 1299)
              O'Dowd,B.F., Nguyen,T., Marchese,A., Cheng,R., Lynch,K.R.,
              Heng,H.H., Kolakowski,L.F. Jr. and George,S.R.
              Discovery of three novel G-protein-coupled receptor genes
              Genomics 47 (2), 310-313 (1998)
PUBMED       9479505
AUTHORS      O'Dowd,B.F.
DIRECT SUBMISSION
TITLE        Submitted (03-OCT-1997) Department of Pharmacology, University of
              Toronto, 8 Taddle Creek Rd., Toronto, ON M5S 1A8, Canada
JOURNAL
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QY      601 AGGCCACCCACCGAGCTGGGGCAGGACGACCCGCAAGGCTTAAACGATGTCTGG 660
DB      814 AGGCCACCCACCGAGCTGGGGCAGGACGACCCGCAAGGCTTAAACGATGTCTGG 873
QY      661 GCCAACCTCTGGTGTCTGCTGCTTCTGCTCCCTGACGCTGGGGCTGACAGTGGCG 720
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QY      841 AAGGAGTTCAGAGGCGCTGTGCTGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900
DB      1054 AAGGAGTTCAGAGGCGCTGTGCTGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1113
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ACCESSION     AKI172786
VERSION       AKI172786.1 GI:47077780
KEYWORDS      oligo capping; fis (full insert sequence).
SOURCE        Homo sapiens (human)
ORGANISM      Homo sapiens
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              Homnidae; Homo.
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              Kawakami,T., Noguchi,S., Itoh,T., Shigeta,K., Senba,T.,
              Matsumura,K., Nakajima,Y., Mizuno,T., Morinaga,M., Ota,T.,
              Suzuki,Y., Obayashi,M., Nishi,T., Shibahara,T., Tanaka,T.,
              Nakamura,Y., Isogai,T. and Sugano,S.
              NEDO human cDNA sequencing project
              Unpublished
              2 (bases 1 to 2270)
              Sugano,S. and Suzuki,Y.
              Direct Submission
              Submitted (22-APR-2004) Sumio Sugano, Institute of Medical Science,
              University of Tokyo, Laboratory of Genome Structure, Human Genome
              Center, Shirokane-dai, 4-6-1, Minato-Ku, Tokyo 108-8639, Japan
              (E-mail:flcdna@mail.ims.u-tokyo.ac.jp, Tel:81-3-5449-5286,
              Fax:81-3-5449-5416)
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## COMMENT

NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing; Research Association for Biotechnology; cDNA library construction; 5'- & 3'-end one pass sequencing; Department of Virology and Human Genome Center, Institute of Medical Science, University of Tokyo (partly supported by Science and Technology Agency).

## FEATURES

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HTG; HTGS\_PHASE1; HTGS\_DRAFT; HTGS\_FULLTOP.  
KEYWORDS  
Homo sapiens (human)  
ORGANISM  
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Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
Waterston.R.H.  
TITLE  
The sequence of Homo sapiens clone  
JOURNAL  
Unpublished  
REFERENCE  
2 (bases 1 to 169391)  
Waterston.R.H.  
TITLE  
Direct Submission  
JOURNAL  
Submitted (18-FEB-2002) Genome Sequencing Center, Washington  
University School of Medicine, 444 Forest Park Parkway, St. Louis,  
MO 63108, USA  
REFERENCE  
3 (bases 1 to 169391)  
Waterston.R.H.  
TITLE  
Direct Submission  
JOURNAL  
Submitted (20-JUN-2002) Genome Sequencing Center, Washington  
University School of Medicine, 444 Forest Park Parkway, St. Louis,  
MO 63108, USA  
COMMENT  
On Jun 14, 2002 this sequence version replaced gi:18699976.  
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Center: Washington University Genome Sequencing Center  
Center code: WUGSC  
Web site: http://genome.wustl.edu/gsc/index.shtml  
Contact: submissions@wustl.edu  
----- Project Information -----  
Center project name: H.FH0511H14  
----- Summary Statistics -----  
Sequencing vector: M13; 0%  
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Chemistry: Dye-primer ET; 0% of reads  
Assembly: Dye-terminator Big Dye; 100% of reads  
Consensus quality: 167477 bases at least Q40  
Consensus quality: 168018 bases at least Q30  
Consensus quality: 168194 bases at least Q20  
Insert size: 185000; agarose-fp  
Insert size: 168791; sum-of-contigs  
Quality coverage: 9.18 in Q20 bases; agarose-fp  
Quality coverage: 9.60 in Q20 bases; sum-of-contigs  
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\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 7 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence



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|                           | <1..>930  |   |
| CDS                       | /product="G-protein coupled receptor 35"  |   |
|                           | 1..930  |   |
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| ORIGIN                    |   |   |
| Query Match               | 99.0%; Score 920.4; DB 8; Length 930;   |   |
| Best Local Similarity     | 99.4%; Pred. No. 4.9e-120;  |   |
| Matches 924; Conservative | 0; Mismatches 6; Indels 0; Gaps 0;  |   |
| QY                        | 1   | ATGAATGGGCACTTACAACTGTGGCTCAGCGACTCACTTGGCCCCCAGCGATCAAG 60         |
| Db                        | 1   | ATGAATGGGCACTTACAACTGTGGCTCAGCGACTCACTTGGCCCCCAGCGATCAAG 60         |
| QY                        | 61  | CTGGGCTTCTACGCCCTACTTGGCGGCTCTGCTGGTGTAGGCTGTGCTCAACAGCCCTG 120     |
| Db                        | 61  | CTGGGCTTCTACGCCCTACTTGGCGGCTCTGCTGGTGTAGGCTGTGCTCAACAGCCCTG 120     |
| QY                        | 121   | GCCTCTGGGTGTCTGCTGCCGATCAGCAGTGGAGAGACCGGATCTTACATGACC 180          |
| Db                        | 121   | GCCTCTGGGTGTCTGCTGCCGATCAGCAGTGGAGAGACCGGATCTTACATGACC 180          |
| QY                        | 181   | AACCTGGCGGTGGCGACTCTGCTGTGTGTGCACTTGGCCCTTGTGTGCACTCCCTG 240        |
| Db                        | 181   | AACCTGGCGGTGGCGACTCTGCTGTGTGTGCACTTGGCCCTTGTGTGCACTCCCTG 240        |
| QY                        | 241   | CGAGACACCTCAGACAGCGCGTGTGCCAGCTCTCCAGGGCATCTACCTGACCAACAG 300       |
| Db                        | 241   | CGAGACACCTCAGACAGCGCGTGTGCCAGCTCTCCAGGGCATCTACCTGACCAACAG 300       |
| QY                        | 301   | TACATGAGCATCAGCTGTGTGCGGCTCAGCGGCATCGCGTGTGCGCGTGTGCGGCGAC 360      |
| Db                        | 301   | TACATGAGCATCAGCTGTGTGCGGCTCAGCGGCATCGCGTGTGCGCGTGTGCGGCGAC 360      |
| QY                        | 361   | CGCTCGTGTGCGCGGCTGTGCGTGTGCGGCTGTGCGGCTGTGCGGCTGTGCGGCTGT 420       |
| Db                        | 361   | CGCTCGTGTGCGCGGCTGTGCGTGTGCGGCTGTGCGGCTGTGCGGCTGTGCGGCTGT 420       |
| QY                        | 421   | TGGGTCTGTGTATCGGCTCCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 480      |
| Db                        | 421   | TGGGTCTGTGTATCGGCTCCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 480      |
| QY                        | 481   | TTCTGTCTTACAGGACACCGGCGCAATTTCAATCTCATGCGGTTCCTGCTGTGCGATTTC 540    |
| Db                        | 481   | TTCTGTCTTACAGGACACCGGCGCAATTTCAATCTCATGCGGTTCCTGCTGTGCGATTTC 540    |
| QY                        | 541   | TACCTGCCCTTGGCGT 600      |
| Db                        | 541   | TACCTGCCCTTGGCGT 600      |
| QY                        | 601   | AGGCGACCCACCGACTGGGGGAGGAGAGCCACCGGAGGCTAAAAGCATGTGTCTGG 660        |
| Db                        | 601   | AGGCGACCCACCGACTGGGGGAGGAGAGCCACCGGAGGCTAAAAGCATGTGTCTGG 660        |
| QY                        | 661   | GCCAACTCTCTGT 720       |
| Db                        | 661   | GCCAACTCTCTGT 720       |
| QY                        | 721   | CTCGCAGTGGGCTGGAAAGCGCTGTGCTCTCTGGAGAGATCGTCGCGCCCTGTACATA 780      |
| Db                        | 721   | CTCGCAGTGGGCTGGAAAGCGCTGTGCTCTCTGGAGAGATCGTCGCGCCCTGTACATA 780      |
| QY                        | 781   | ACCAGCAAGCTCTCAGATGCCAACTGTGCTGCGCTGGAGCGCATCTGCTACTACTACATGGCC 840 |
| Db                        | 781   | ACCAGCAAGCTCTCAGATGCCAACTGTGCTGCGCTGGAGCGCATCTGCTACTACTACATGGCC 840 |
| QY                        | 841   | AAGGAGTTCCAGGAGCGCTGTGCACTGGCCGCTGGCTCCCGCTGCTAAAGCCCAAAAAGC 900    |
| Db                        | 841   | AAGGAGTTCCAGGAGCGCTGTGCACTGGCCGCTGGCTCCCGCTGCTAAAGCCCAAAAAGC 900    |
| QY                        | 901   | CAGGACTCTCTGTGCGTGAACCTCGCCTAA 930                                  |
| Db                        | 901   | CAGGACTCTCTGTGCGTGAACCTCGCCTAA 930                                  |
| RESULT 7                  |   |   |
| LOCUS                     | CR541765 930 bp mRNA linear PRI 29-JUN-2004   |   |
| DEFINITION                | Homo sapiens full open reading frame cDNA clone RZPD0834D0330D for  |   |
|                           | gene GPR35, G protein-coupled receptor 35; complete cds, incl.  |   |
|                           | stopcodon.  |   |
| ACCESSION                 | CR541765  |   |
| VERSION                   | CR541765.1 GI:49456486  |   |
| KEYWORDS                  | Full ORF shuttle clone, Gateway(TM), complete cds.  |   |
| SOURCE                    | Homo sapiens (human)  |   |
| ORGANISM                  | Homo sapiens  |   |
| REFERENCE                 | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;   |   |
| AUTHORS                   | Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;   |   |
|                           | Hominidae; Homo.  |   |
|                           | 1 (bases 1 to 930)  |   |
|                           | Halleck,A., Ebert,L., Moundinya,M., Schick,M., Eisenstein,S.,   |   |
|                           | Neubert,P., Katrang,K., Schatten,R., Shen,B., Henze,S., Mar,W.,   |   |
|                           | Korn,B., Zuo,D., Hu,Y. and LaBaer,J.  |   |
|                           | Cloning of human full open reading frames in Gateway(TM) system   |   |
|                           | entry vector (pDONR201)   |   |
|                           | Unpublished   |   |
| JOURNAL                   | 2 (bases 1 to 930)  |   |
| REFERENCE                 | Halleck,A., Ebert,L., Moundinya,M., Schick,M., Eisenstein,S.,   |   |
| AUTHORS                   | Neubert,P., Katrang,K., Schatten,R., Shen,B., Henze,S., Mar,W.,   |   |
|                           | Korn,B., Zuo,D., Hu,Y. and LaBaer,J.  |   |
|                           | Direct Submission   |   |
| TITLE                     | Submitted (28-JUN-2004) RZPD Deutsches Ressourcenzentrum fuer   |   |
| JOURNAL                   | Genomforschung GmbH, Im Neuenheimer Feld 580, D-69120 Heidelberg,   |   |
|                           | Germany   |   |
| COMMENT                   | RZPD: RZPD0834D0330D, ORFNO 3528  |   |
|                           | www.rzpd.de/cgi-bin/products/cl.cgi?cloneID=RZPD0834D0330D RZPDLIB;   |   |
|                           | Human Full ORF Clones Gateway(TM) - RZPD (kan-resist.) RZPD LIB No.   |   |
|                           | 834   |   |
|                           | www.rzpd.de/cgi-bin/products/showLib.pl.cgi/response?libNo=834  |   |
|                           | www.rzpd.de/products/orfclones/   |   |
|                           | Contact: Inge Ariart  |   |
|                           | RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH,  |   |
|                           | Heubnerweg 6, D-14059 Berlin, Germany   |   |
|                           | Tel: +49 30 32639 100   |   |
|                           | Fax: +49 30 32639 111   |   |
|                           | www.rzpd.de   |   |
|                           | This clone is available from RZPD;  |   |
|                           | Contact RZPD (customer.service@rzpd.de) for further information.  |   |
|                           | Clone name at Harvard Institute of Proteomics   |   |
|                           | (www.hip.harvard.edu: FLH13100.01X  |   |
|                           | This CDS clone is part of a collection of human full ORF clones   |   |
|                           | jointly established and verified by the Harvard Institute of  |   |
|                           | Proteomics (HIP) and RZPD.  |   |
|                           | This CDS has been cloned incl. stopcodon.   |   |
|                           | The CDS has been inserted into pDONR201 via a BP Clonase(TM)  |   |
|                           | reaction. Additional sequence has been added in front of the start  |   |
|                           | codon: att..AAAAA GCA GGC TCC ATG (ATG).  |   |
|                           | The stopcodon is followed by the 3' att site: GACCAGCTTTCTT..att  |   |
|                           | The clone is validated by full sequence check.  |   |
|                           | Compared to the reference sequence NM_005301 (GI:33695096) we found   |   |



|   |                       |  |               |               |                   |
|---|-----------------------|--|---------------|---------------|-------------------|
| AA exchange(s) at position (first base of changed triplet): |                       |  |               |               |                   |
| 890(ser->arg)   |                       |  |               |               |                   |
| Clone distribution: http://www.rzpd.de/products/orfclones/. |                       |  |               |               |                   |
| <b>FEATURES</b>   |                       |  |               |               |                   |
| source  | Location/Qualifiers   |  |               |               |                   |
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|   |                       | /clone_lib="Human Full ORF Clones Gateway(TM) - RZPD"  |               |               |                   |
|   |                       | /lab_host="DH5Alpha"   |               |               |                   |
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|   |                       | /translation="MNGYTNCCSSDLTWPPAIKLGFYAVLGVLLVGLLLNSLALMVFCRCMQWTRITRYIMTNLAADLCCLTFELVLSLRDTSDTFLCSQSIYLTNRYMSILVTAIAVDVVAVNHPLRAKLRSRQAAAACVALVWLVIIGSLVARWLLGTQEGGPCRSTPHFNNSAFPLLGFLVLAVVPFSLKVVTALAORPTDVGOAARTRKAARMVWANLVVFVCFLPLHLVGLTVRLAVGNACALLETRIRALIYTSKLSDANCCLDAICYYYMAKFQEQEASALAVAPRAKAHKHSQDSLCVTLA" |               |               |                   |
| <b>ORIGIN</b>   |                       |  |               |               |                   |
|   | Query Match           | 99.0%;   | Score         | 920.4;        | DB 8; Length 930; |
|   | Best Local Similarity | 99.4%;   | Pred.         | No. 4.9e-120; |                   |
|   | Matches 924;          | Conservative 0;  | Mismatches 6; | Indels 0;     | Gaps 0;           |
| Qy  | 1                     | ATGAATGGCACCTACAACACCGTGCGCTGCCAGCACTTCACCTGGCCCCCAGCGCATCAAG  | 60            |               |                   |
| Dd  | 1                     | ATGAATGGCACCTACAACACCGTGCGCTGCCAGCACTTCACCTGGCCCCCAGCGCATCAAG  | 60            |               |                   |
| Qy  | 61                    | CTGGGCTTTACGCCTACTTGGGGCGTCCTGCTGTGTGTAGCCCTGCTGCTCAAAGCGCTG   | 120           |               |                   |
| Dd  | 61                    | CTGGGCTTTACGCCTACTTGGGGCGTCCTGCTGTGTGTAGCCCTGCTGCTCAAAGCGCTG   | 120           |               |                   |
| Qy  | 121                   | GCGCTCTGGGGTGTCTGCTGCCGATGCAGCAGTGGACGGAGACC CGCATCTACATGACC   | 180           |               |                   |
| Dd  | 121                   | GCGCTCTGGGGTGTCTGCTGCCGATGCAGCAGTGGACGGAGACC CGCATCTACATGACC   | 180           |               |                   |
| Qy  | 181                   | AACCTGGCGGTGGCGACCTCTGCTGTGTGCACCTTTGCCCTTCGTGTGCTGCTGCTG  | 240           |               |                   |
| Dd  | 181                   | AACCTGGCGGTGGCGACCTCTGCTGTGTGCACCTTTGCCCTTCGTGTGCTGCTGCTG  | 240           |               |                   |
| Qy  | 241                   | CGAGACACTCAGACACGCCGCTGTGCCAGCTCTCTCCAGGGGCATCTACCTGACCMACAGG  | 300           |               |                   |
| Dd  | 241                   | CGAGACACTCAGACACGCCGCTGTGCCAGCTCTCTCCAGGGGCATCTACCTGACCMACAGG  | 300           |               |                   |
| Qy  | 301                   | TACATGAGCATCAGCTGGTTCACGGCCATCGCGTGGACCGCTATGTGGCGTGGCGGAC   | 360           |               |                   |
| Dd  | 301                   | TACATGAGCATCAGCTGGTTCACGGCCATCGCGTGGACCGCTATGTGGCGTGGCGGAC   | 360           |               |                   |
| Qy  | 361                   | CCGCTGGCTGCCC GGCGCTCGGGTCCCCCAGGAGCGTGGCGCGTGTGGCGGTCCTC  | 420           |               |                   |
| Dd  | 361                   | CCGCTGGCTGCCC GGCGCTCGGGTCCCCCAGGAGCGTGGCGCGTGTGGCGGTCCTC  | 420           |               |                   |
| Qy  | 421                   | TGGGTGCTGTGTCATCGGCTCCCTGGTGTGCTCGCTGGGATTTCAGAGGGCGGCG  | 480           |               |                   |
| Dd  | 421                   | TGGGTGCTGTGTCATCGGCTCCCTGGTGTGCTCGCTGGGATTTCAGAGGGCGGCG  | 480           |               |                   |
| Qy  | 481                   | TTCTGCTTCAGAGACACCGGCACAAATTTCAACTCCATGCGGTTCGCCGCTGCTGGATT  | 540           |               |                   |
| Dd  | 481                   | TTCTGCTTCAGAGACACCGGCACAAATTTCAACTCCATGCGGTTCGCCGCTGCTGGATT  | 540           |               |                   |
| Qy  | 541                   | TACCTGCCCTTGCCGCTGGTGTCTTCTGCTCCCTGAAAGGTGGTGACTGCCCTGGCCCG  | 600           |               |                   |
| Dd  | 541                   | TACCTGCCCTTGCCGCTGGTGTCTTCTGCTCCCTGAAAGGTGGTGACTGCCCTGGCCCG  | 600           |               |                   |
| Qy  | 601                   | AGGCCACCCACCGACGTGGGGCAGGCAGAGGCCACCCCGCAAGGCTAAACGATGTCTGG  | 660           |               |                   |

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FCFRSTRHFNPSAPFLGLFPLAVVVFSLKVVLTALAQRPPTDVGQAEATRAARM  
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ORIGIN

Query Match 99.0%; Score 920.4; DB 11; Length 930;  
Best Local Similarity 99.4%; Pred. No. 4.9e-120;  
Matches 924; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 ATGAATGGGACCTACACACCTGTGGCTCCAGGACCTACCTGCGCCCGCCGATCAAG 60  
DB 1 ATGAATGGGACCTACACACCTGTGGCTCCAGGACCTACCTGCGCCCGCCGATCAAG 60

QY 61 CTGGGCTTCTACCGCTACTTGGGCGTCTCTGCTGGTGTAGGCTGTCTCAACAGCCTG 120  
DB 61 CTGGGCTTCTACCGCTACTTGGGCGTCTCTGCTGGTGTAGGCTGTCTCAACAGCCTG 120

QY 121 GCGCTCTGGGTGTCTGTGCTCCGATGACAGATGAGAGACCCGATCTACATGACC 180  
DB 121 GCGCTCTGGGTGTCTGTGCTCCGATGACAGATGAGAGACCCGATCTACATGACC 180

QY 181 AACCTGGCGTGGCGGACCTTGCCTGTGTGACCTTGCCTTCTGCTGCACTCCCTG 240  
DB 181 AACCTGGCGTGGCGGACCTTGCCTGTGTGACCTTGCCTTCTGCTGCACTCCCTG 240

QY 241 CGAGACACCTCAGACACCGCGTGTGCAGCTCTCCAGGGACCTACCTGACCAACAGG 300  
DB 241 CGAGACACCTCAGACACCGCGTGTGCAGCTCTCCAGGGACCTACCTGACCAACAGG 300

QY 301 TACATGAGCATCAGCTGTGTACGGCCATGCGCGTGAACGCTATGTGCGCGTGGAC 360  
DB 301 TACATGAGCATCAGCTGTGTACGGCCATGCGCGTGAACGCTATGTGCGCGTGGAC 360

QY 361 CGGCTGGTGGCGCGGCTGGCGTCCCGAGGACGCTGCGCGTGGCGGTCCTC 420  
DB 361 CGGCTGGTGGCGCGGCTGGCGTCCCGAGGACGCTGCGCGTGGCGGTCCTC 420

QY 421 TGGGTGTGTGTATCGGCTCCCTGTGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 480  
DB 421 TGGGTGTGTGTATCGGCTCCCTGTGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 480

QY 481 TTCTGTCTCAGGAGCACCGGACCAATTTCAATCCATGCGGTTCCCGCTGCTGGATTC 540  
DB 481 TTCTGTCTCAGGAGCACCGGACCAATTTCAATCCATGCGGTTCCCGCTGCTGGATTC 540

QY 541 TACCTGCGCTGGCGCTGT 600  
DB 541 TACCTGCGCTGGCGCTGT 600

QY 601 AGGCGACCCACCAAGCTGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 660  
DB 601 AGGCGACCCACCAAGCTGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 660

QY 661 GCGAACTCTGT 720  
DB 661 GCGAACTCTGT 720

QY 721 CTGCGAGTGGGCTGGAAACGCTGTGCGCTCTGGAGACGATCGTGGCGGCTGTACATA 780  
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QY 781 ACCAGCAAGCTCTCAGATGCCAATCTGTGCTGGAGCGCATCTGTACTACTACATGGCC 840  
DB 781 ACCAGCAAGCTCTCAGATGCCAATCTGTGCTGGAGCGCATCTGTACTACTACATGGCC 840

QY 841 AAGGAGTTCAGAGGCGTCTGCACTGGCGCGTGGCTCCCGTGTCTAAGGCCCAAAAGC 900  
DB 841 AAGGAGTTCAGAGGCGTCTGCACTGGCGCGTGGCTCCCGTGTCTAAGGCCCAAAAGC 900

QY 901 CAGGACTCTCTGT 930  
DB 901 CAGGACTCTCTGT 930

RESULT 9  
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LOCUS ARI53299 1875 bp DNA linear PAT 08-AUG-2001  
DEFINITION Sequence 21 from patent US 6235481.  
ACCESSION ARI53299  
VERSION ARI53299.1 GI:15120831  
KEYWORDS .  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 1875)  
AUTHORS Horikawa, Y., Oda, N., Hanis, C.L., Bell, G.I. and Cox, N.J.  
TITLE Polynucleotides encoding calpain 10  
JOURNAL Patent: US 6235481-A 21-22-MAY-2001;  
FEATURES  
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ORIGIN

Query Match 99.0%; Score 920.4; DB 6; Length 1875;  
Best Local Similarity 99.4%; Pred. No. 4.2e-120;  
Matches 924; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 ATGAATGGGACCTACACACCTGTGGCTCCAGGACCTACCTGCGCCCGCCGATCAAG 60  
DB 576 ATGAATGGGACCTACACACCTGTGGCTCCAGGACCTACCTGCGCCCGCCGATCAAG 635

QY 61 CTGGGCTTCTACCGCTACTTGGGCGTCTCTGCTGGTGTAGGCTGTCTGCTCAACAGCCTG 120  
DB 636 CTGGGCTTCTACCGCTACTTGGGCGTCTCTGCTGGTGTAGGCTGTCTGCTCAACAGCCTG 695

QY 121 GCGCTCTGGGTGTCTGTGCTGGCGATGACAGATGAGAGACCCGATCTACATGACC 180  
DB 696 GCGCTCTGGGTGTCTGTGCTGGCGATGACAGATGAGAGACCCGATCTACATGACC 755

QY 181 AACCTGGGCGTGGCGGACCTCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 240  
DB 756 AACCTGGGCGTGGCGGACCTCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 815

QY 241 CGAGACACCTCAGACACCGCGTGTGCGAGCTCTCCAGGGCATCTACCTGACCAACAGG 300  
DB 816 CGAGACACCTCAGACACCGCGTGTGCGAGCTCTCCAGGGCATCTACCTGACCAACAGG 875

QY 301 TACATGAGCATCAGCTGTGTGTCAGGCGCATCGCGTGGAGCGGATGTGGCGGTGGGAC 360  
DB 876 TACATGAGCATCAGCTGTGTGTCAGGCGCATCGCGTGGAGCGGATGTGGCGGTGGGAC 935

QY 361 CGGCTGGTGGCGCGGCTGGCGTCCCGAGGAGGCTGCGGCGCTGTGCGCGGTCTTC 420  
DB 936 CGGCTGGTGGCGCGGCTGGCGTCCCGAGGAGGCTGCGGCGCTGTGCGCGGTCTTC 995

QY 421 TGGGTGTGTGTATCGGCTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 480  
DB 996 TGGGTGTGTGTATCGGCTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1055

QY 481 TTCTGTCTTCAGGAGCACCGGACCAATTTCAACTCCATGCGGTTCCCGCTGCTGGATTC 540  
DB 1056 TTCTGTCTTCAGGAGCACCGGACCAATTTCAACTCCATGCGGTTCCCGCTGCTGGATTC 1115

QY 541 TACCTGCGCTGGCGCTGT 600  
DB 1116 TACCTGCGCTGGCGCTGT 1175

QY 601 AAGGCCACCCACCAAGCTGTGGGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 660  
DB 1176 AAGGCCACCCACCAAGCTGTGGGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1235



576 ATGATGGCACCTACAAACCTGTGGCTCCAGGACCTCACCTGGCCCCCAGCGATCAAG 635  
61 CTGGGCTTCTACGCTTACTTGGGGTCTCTGTGGTGTAGGCTGTGCTCAACAGCCTG 120  
636 CTGGGCTTCTACGCTTACTTGGGGTCTCTGTGGTGTAGGCTGTGCTCAACAGCCTG 695  
121 GCCTCTGGGTGTCTGCTGCGCATGACAGTGTGAGGAGACCGCATCTACATGACC 180  
696 GCCTCTGGGTGTCTGCTGCGCATGACAGTGTGAGGAGACCGCATCTACATGACC 755  
181 AACCTGGCGTGGCGGACCTCTGCTGCTGTGACCTTGGCCCTTCTGCTGCACTCCCTG 240  
756 AACCTGGCGTGGCGGACCTCTGCTGCTGTGACCTTGGCCCTTCTGCTGCACTCCCTG 815  
241 CGAGACCTCTAGACAGCGCGTGTGCGCAGCTTCCAGGGCATCTACCTGACCAACAGG 300  
816 CGAGACCTCTAGACAGCGCGTGTGCGCAGCTTCCAGGGCATCTACCTGACCAACAGG 875  
301 TACATGAGCATCAGCCTGTGTCAGGCGCATCGCGTGGACCGCTATGTGGCCGTGGGCAC 360  
876 TACATGAGCATCAGCCTGTGTCAGGCGCATCGCGTGGACCGCTATGTGGCCGTGGGCAC 935  
361 CCCTCTGGTCCCGCGGCTGCGGCTCCCGCAGGAGGCTCGCGCGGTGCGCGTCCCTC 420  
936 CCCTCTGGTCCCGCGGCTGCGGCTCCCGCAGGAGGCTCGCGCGGTGCGCGTCCCTC 995  
421 TGGGTGTGTCTATCGGCTCCCTGTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480  
996 TGGGTGTGTCTATCGGCTCCCTGTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1055  
481 TTCTGCTTCAAGGAGCAGCGGCGCAATTTCAATCCATGCGGTTCCTGCTGCTGCTGCTG 540  
1056 TTCTGCTTCAAGGAGCAGCGGCGCAATTTCAATCCATGCGGTTCCTGCTGCTGCTGCTG 1115  
541 TACTTGGCTTGGCGTGGTGTGCTTCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600  
1116 TACTTGGCTTGGCGTGGTGTGCTTCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1175  
601 AGGCCACCCACCGAGTGGGGCAGGAGGCCACCGCAGGCTAAACCGCATGTGCTGG 660  
1176 AGGCCACCCACCGAGTGGGGCAGGAGGCCACCGCAGGCTAAACCGCATGTGCTGG 1235  
661 GCCAATCTCTGTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720  
1236 GCCAATCTCTGTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1295  
721 CTGCGAGTGGGCTGGAACGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780  
1296 CTGCGAGTGGGCTGGAACGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1355  
781 ACCAGCAAGCTCTCAGATGCCAATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840  
1356 ACCAGCAAGCTCTCAGATGCCAATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1415  
841 AAGGAGTTCAGAGGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900  
1416 AAGGAGTTCAGAGGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1475  
901 CAGGACTCTCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 930  
1476 CAGGACTCTCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1505

## RESULT 12

AF089087  
LOCUS AF089087  
DEFINITION Homo sapiens G protein-coupled receptor mRNA, complete cds.  
ACCESSION AF089087  
VERSION AF089087.1 GI:10503932  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominiidae; Homo.  
1 (bases 1 to 1875)  
Horikawa, Y., Oda, N., Cox, N.J., Li, X., Orho-Melander, M., Hara, M.,  
Hinokio, Y., Lindner, T.H., Mashima, H., Schwarz, P.E., del  
Rosque-Plata, L., Horikawa, Y., Oda, Y., Yoshiuchi, I., Colilla, S.,  
Polonsky, K.S., Wei, S., Concannon, P., Iwasaki, N., Schulse, J., and  
Baier, L.J., Bogardus, C., Groop, L., Boerwinkle, E., Hanis, C.U. and  
Bell, G.I.  
Genetic variation in the gene encoding calpain-10 is associated  
with type 2 diabetes mellitus  
Nat. Genet. 26 (2), 163-175 (2000)  
11017071  
2 (bases 1 to 1875)  
Horikawa, Y. and Bell, G.I.  
Direct Submission  
Submitted (02-SEP-1998) Howard Hughes Medical Institute, The  
University of Chicago, 5841 S. Maryland Avenue, MC1028, Chicago, IL  
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with type 2 diabetes mellitus
JOURNAL Nat. Genet. 26 (2), 163-175 (2000)
PUBMED 11017071
REFERENCE 2 (bases 1 to 65674)
AUTHORS Horikawa, Y.
TITLE Direct Submission
JOURNAL Submitted (17-MAR-1999) The University of Chicago, Howard Hughes
Medical Institute, 5841 S. Maryland Avenue MC1028, Chicago,
Illinois 60637, USA
REFERENCE 3 (bases 1 to 65674)
AUTHORS Horikawa, Y.
TITLE Direct Submission
JOURNAL Submitted (19-JAN-2001) The University of Chicago, Howard Hughes
Medical Institute, 5841 S. Maryland Avenue MC1028, Chicago,
Illinois 60637, USA
REMARK Sequence update by submitter
REFERENCE 4 (bases 1 to 65674)
AUTHORS Horikawa, Y.
TITLE Direct Submission
JOURNAL Submitted (22-APR-2002) The University of Chicago, Howard Hughes
Medical Institute, 5841 S. Maryland Avenue MC1028, Chicago,
Illinois 60637, USA
REMARK Sequence update by submitter
COMMENT On Apr 22, 2002 this sequence version replaced gi:12313882.
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Job time : 5119 secs

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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 11, 2006, 00:25:50 ; Search time 684 Seconds  
(without alignments)  
9061.643 Million cell updates/sec

Title: US-10-083-168-84

Perfect score: 930

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Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N Geneseq 21.\*

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- 14: geneseqn2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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## ALIGNMENTS

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ID ABST73401 standard; DNA; 930 BP.

AC ABST73401;

DT 04-DEC-2002 (first entry)

DE DNA encoding human GPCR GPR35 mutant A216K.

Human; transmembrane receptor; G-protein coupled receptor; GPCR; allergy; hypertension; reflux disease; depression; migraine; schizophrenia; ulcer; psychotic disorder; asthma; bronchospasm; anaesthesia; myocardial infarction; MI; stroke; glaucoma; anxiety; prostatic hyperplasia; epilepsy; prostate cancer; rhinitis; angina; prostatic hypertrophy; mutant; ds.

OS Homo sapiens.

OS Synthetic.

PN WO200268600-A2.

PD 06-SEP-2002.

PF 26-FEB-2002; 2002WO-US005625.

PR 26-FEB-2001; 2001US-0271913P.

PA (AREN-) ARENA PHARM INC.

PI Liaw CW, Chalmers DT, Behan DP, Maciejewski-Lenior D, Leonard JN;

PI Lin I, Ortuno D;

DR WPI; 2002-706980/76.

DR P-PSDB; ABG95172.

XX New human G-protein coupled receptor (GPCR), useful for screening agonist or inverse agonist compounds for treating diseases associated with GPCR.

PT Example 2; Page 188-189; 201pp; English.

PS The present invention relates to transmembrane receptors, particularly

CC

|    |   |  |
|----|---|--|
| CC | endogenous human G-protein coupled receptors (GPCRs), mutant (non-        |  |
| CC | endogenous) versions of the GPCRs, and the polynucleotide sequences       |  |
| CC | encoding them. The GPCRs are useful for screening agonist or inverse      |  |
| CC | agonist compounds for treating diseases associated with GPCR. Diseases    |  |
| CC | that can be treated with such compounds include allergies, hypertension,  |  |
| CC | reflux disease, depression, migraine, schizophrenia, ulcers, psychotic    |  |
| CC | disorders, asthma, bronchospasm, anaesthesia, myocardial infarction (MI), |  |
| CC | stroke, glaucoma, prostatic hyperplasia, epilepsy, prostate cancer,       |  |
| CC | anxiety, prostatic hypertrophy, rhinitis, and angina. The present         |  |
| CC | sequence encodes a mutant human GPCR                                      |  |
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| Qy | 361 CCGCTGCGTGC CCGCGGCTGCGGTCCCGCAGGACGGCTGCGCGCTGTGTGCGCGTCTCTC 420     |  |
| Db | 361 CCGCTGCGTGC CCGCGGCTGCGGTCCCGCAGGACGGCTGCGCGCTGTGTGCGCGTCTCTC 420     |  |
| Qy | 421 TGGGTGCTGTGTCATCGGCTCCCTGGTGTGCTCGCTGGCTCTCTGGGATTCAGGAGGGCGGC 480    |  |
| Db | 421 TGGGTGCTGTGTCATCGGCTCCCTGGTGTGCTCGCTGGCTCTCTGGGATTCAGGAGGGCGGC 480    |  |
| Qy | 481 TTCTGTCTTCAGGACACCGGCGCAAA TTTCAACTCCATGCGGTTCCCGCTCTGGGATTC 540      |  |
| Db | 481 TTCTGTCTTCAGGAGACA CCGGCGCAAA TTTCAACTCCATGCGGTTCCCGCTCTGGGATTC 540   |  |
| Qy | 541 TACCTGCCCCCTGGCGGTGGTCTTCTGTGCTCCCTGAAAGTGTGTGACTGCCCTCGCCCCAG 600    |  |
| Db | 541 TACCTGCCCCCTGGCGGTGGTCTTCTGTGCTCCCTGAAAGTGTGTGACTGCCCTCGCCCCAG 600    |  |
| Qy | 601 AGGCCACCCACAGCATGTGGGCGACGACAGAGCCACCCGCAAGGCTAAACGATGGTCTGG 660      |  |
| Db | 601 AGGCCACCCACAGCATGTGGGCGACGACAGAGCCACCCGCAAGGCTAAACGATGGTCTGG 660      |  |
| Qy | 661 GCCAACTCTGTGTTCTGTGTTCTGTTCTGCTGCTGCTGCACTGGGGCTGACAGTGGC 720         |  |
| Db | 661 GCCAACTCTGTGTTCTGTGTTCTGTTCTGCTGCTGCTGCACTGGGGCTGACAGTGGC 720         |  |
| Qy | 721 CTCGACGTGGGCTGGAAAGCCTGTGTCCTCTCTGGAGACGATCCGCTGCGCCCTGTACATA 780     |  |
| Db | 721 CTCGACGTGGGCTGGAAAGCCTGTGTCCTCTCTGGAGACGATCCGCTGCGCCCTGTACATA 780     |  |
| Qy | 781 ACAGCAAGCTCTCAGATGCCAATCTGTGCTGTGACCGCCATCTGTGTACTATCATGCGCC 840      |  |
| Db | 781 ACCAGCAAGCTCTCAGATGCCAATCTGTGCTGTGACCGCCATCTGTGTACTATCATGCGCC 840     |  |



```
Db 121 GCGCTCTGGGTGTTCTGTCGCGATGACAGAGTGGAGCGAGACCGCATCTACATGACC 180
Qy 181 AACCTGGCGGTGGCCGACCTCTGCTGTCTGTGCACTTGGCCCTTGTGTGCACTCCCTG 240
Db 181 AACCTGGCGGTGGCCGACCTCTGCTGTCTGTGCACTTGGCCCTTGTGTGCACTCCCTG 240
Qy 241 CGAGACACCTCAGACAGCGCGCTGTGCGAGCTCTCCAGGGCATCTACCTGACCAACAG 300
Db 241 CGAGACACCTCAGACAGCGCGCTGTGCGAGCTCTCCAGGGCATCTACCTGACCAACAG 300
Qy 301 TACATGAGCATCAGCTGTGTCAAGGCGCATCGCGGTGACCGCTATGTGGCGCTGCGGCAC 360
Db 301 TACATGAGCATCAGCTGTGTCAAGGCGCATCGCGGTGACCGCTATGTGGCGCTGCGGCAC 360
Qy 361 CCGCTGCTGCCGCGCGCTGCGGTGCGGTGCGGTGCGGTGCGGTGCGGTGCGGTGCGGT 420
Db 361 CCGCTGCTGCCGCGCGCTGCGGTGCGGTGCGGTGCGGTGCGGTGCGGTGCGGTGCGGT 420
Qy 421 TGGGTGCTGCTCATCGGCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
Db 421 TGGGTGCTGCTCATCGGCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
Qy 481 TTCTGCTTCAAGGACACCGCGCAAAATTTCAAATTCATGCGGTTCGCGCTGCTGGATTC 540
Db 481 TTCTGCTTCAAGGACACCGCGCAAAATTTCAAATTCATGCGGTTCGCGCTGCTGGATTC 540
Qy 541 TACCTGCCCCCTGCGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
Db 541 TACCTGCCCCCTGCGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
Qy 601 AGGCCACCCAGCAGTGGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 660
Db 601 AGGCCACCCAGCAGTGGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 660
Qy 661 GCCAAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
Db 661 GCCAAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
Qy 721 CTCGCAATGGGCTGGAACGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
Db 721 CTCGCAATGGGCTGGAACGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
Qy 781 ACCAGCAAGCTCTCAGATGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
Db 781 ACCAGCAAGCTCTCAGATGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
Qy 841 AAGGAGTTCAGAGGCGCTGCACTGGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
Db 841 AAGGAGTTCAGAGGCGCTGCACTGGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
Qy 901 CAGGACTCTCTGTGCGTGACCTCGGCTAA 930
Db 901 CAGGACTCTCTGTGCGTGACCTCGGCTAA 930
```

## RESULT 4

ADB67672

ID ADB67672 standard; DNA; 930 BP.

XX

AC ADB67672;

XX

DT 04-DEC-2003 (first entry)

XX

DE Human G protein-coupled receptor 35 DNA, SEQ ID 10.

XX

KW Cardiant; Gene therapy; heart failure; gene; ds; human;

XX

OS G protein-coupled receptor 35; receptor.

XX

OS Homo sapiens.

XX

PN WO2003072824-A1.

XX

PD 04-SEP-2003.

XX

PF 27-FEB-2003; 2003WO-JP002228.

XX

PR 28-FEB-2002; 2002JP-00054388.

PR

15-APR-2002; 2002JP-00112228.

XX

(SANY ) SANKYO CO LTD.

XX

Kitakaze M, Takashima S, Asakura M, Isomura T, Furukawa H;

PI

Koishi R, Nakamaru K;

XX

WPI: 2003-679959/64.

DR

P-PSDB; ADB67656.

XX

Predicting pathological conditions in heart failure using marker genes

PT

and proteins.

XX

Claim 1; Page 78; 137pp; Japanese.

PS

The present invention relates to a method for predicting pathological

CC

conditions in heart failure using expression of one of 17 gene sequences

CC

(ADB67663-ADB67678); or protein sequences encoded by the genes (ADB67648-

CC

ADB67662). The proteins and genes are useful for diagnosis, treatment and

CC

prevention of heart failure.

XX

Sequence 930 BP; 138 A; 328 C; 279 G; 185 T; 0 U; 0 Other;

SQ

Query Match

Best Local Similarity 99.5%; Score 925.2; DB 9; Length 930;

Matches 927; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ATGAATGGCACCTACAACACCTGTGGCTCCAGCGACCTCACCTGGCCCCCAGCATCAAG 60

Db

1 ATGAATGGCACCTACAACACCTGTGGCTCCAGCGACCTCACCTGGCCCCCAGCATCAAG 60

Qy

61 CTGGGCTTCTACGCTTACTTGGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120

Db

61 CTGGGCTTCTACGCTTACTTGGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120

Qy

121 GCGCTCTGGGTGTTCTGCTGCGCATGACGACAGTGGAGCGAGACCGGATCTACATGACC 180

Db

121 GCGCTCTGGGTGTTCTGCTGCGCATGACGACAGTGGAGCGAGACCGGATCTACATGACC 180

Qy

181 AACCTGGCGGTGGCGACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240

Db

181 AACCTGGCGGTGGCGACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240

Qy

241 CGAGACACCTCAGACACCGCGCTGTGCCAGCTCTCCAGGGCATCTACCTGACCAACAGG 300

Db

241 CGAGACACCTCAGACACCGCGCTGTGCCAGCTCTCCAGGGCATCTACCTGACCAACAGG 300

Qy

301 TACATGAGCATCAGCTGTGTCAAGGCGCATGCGCGGTGGAGCGGATGTGGCGGCGGAC 360

Db

301 TACATGAGCATCAGCTGTGTCAAGGCGCATGCGCGGTGGAGCGGATGTGGCGGCGGAC 360

Qy

361 CCGCTGCGTGGCGCGGCTGCGGTGCGGTGCGGTGCGGTGCGGTGCGGTGCGGTGCGGTGCG 420

Db

361 CCGCTGCGTGGCGCGGCTGCGGTGCGGTGCGGTGCGGTGCGGTGCGGTGCGGTGCGGTGCG 420

Qy

421 TGGGTGCTGCTCATCGGCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480

Db

421 TGGGTGCTGCTCATCGGCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480

Qy

481 TTCTGCTTCAAGGACACCGCGCAAAATTTCAAATTCATGCGGTTCGCGCTGCTGGATTC 540

Db

481 TTCTGCTTCAAGGACACCGCGCAAAATTTCAAATTCATGCGGTTCGCGCTGCTGGATTC 540

Qy

541 TACCTGCCCCCTGCGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600

Db

541 TACCTGCCCCCTGCGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600

Qy

601 AGGCCACCCAGCAGTGGGGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 660









|   |   |   |  |
|---|---|---|--|
| AAZ50891  |   | Human receptor-associated protein cDNA from Incyte clone 3083742. |  |
| ID  | AAZ50891 standard; cDNA; 1369 BP.   |   |  |
| XX  | AAZ50891;   |   |  |
| XX  | 31-MAY-2000 (first entry)   |   |  |
| DE  | Human receptor-associated protein cDNA from Incyte clone 3083742.         |   |  |
| XX  | Human receptor-associated protein; HRAP; Incyte clone 3083742;            |   |  |
| KW  | cytostatic; immunomodulatory; antiinflammatory; cardiant; antianaemic;    |   |  |
| KW  | antiarteriosclerotic; hepatotropic; antiarthritic antirheumatic;          |   |  |
| KW  | antiasthmatic; osteopathic; antiallergic; antidiabetic; dermatological;   |   |  |
| KW  | neuroprotective; diagnosis; treatment; prevention; reproductive disorder; |   |  |
| KW  | cardiovascular; cell proliferative; autoimmune; inflammatory; allergy;    |   |  |
| KW  | gastrointestinal; atherosclerosis; cirrhosis; leukaemia; cancer; AIDS;    |   |  |
| KW  | arthritis; anaemia; asthma; dermatitis; diabetes; osteoporosis;           |   |  |
| KW  | multiple sclerosis; irritable bowel syndrome; ss.                         |   |  |
| OS  | Homo sapiens.   |   |  |
| XX  |   |   |  |
| XX  | Key Location/Qualifiers   |   |  |
| FT  | CDS 45..974   |   |  |
| FT  | /*tag= a  |   |  |
| FT  | /product= "HRAP"  |   |  |
| XX  |   |   |  |
| XX  | WO200008155-A2.   |   |  |
| PD  | 17-FEB-2000.  |   |  |
| XX  |   |   |  |
| XX  | 06-AUG-1999; 99WO-US017777.   |   |  |
| XX  |   |   |  |
| PR  | 07-AUG-1998; 98US-0160065P.   |   |  |
| PR  | 01-SEP-1998; 98US-0098703P.   |   |  |
| XX  |   |   |  |
| PA  | (INCY-) INCYTE PHARM INC.   |   |  |
| XX  |   |   |  |
| PI  | Hillman JL, Yue H, Lal P, Tang YT, Gorgone GA, Guegler KJ;                |   |  |
| PI  | Corley NC, Baughn MR;   |   |  |
| XX  |   |   |  |
| DR  | WPI; 2000-205710/18.  |   |  |
| DR  | P-PSDB; AAY69989.   |   |  |
| XX  |   |   |  |
| PT  | New human receptor-associated proteins (HRAP) useful for the diagnosis,   |   |  |
| PT  | treatment and prevention of cell proliferative, autoimmune, inflammatory, |   |  |
| PT  | reproductive, cardiovascular, and gastrointestinal disorders.             |   |  |
| XX  |   |   |  |
| PS  | Claim 9; Page 91; 99pp; English.  |   |  |
| XX  |   |   |  |
| CC  | The present sequence is a cDNA encoding human receptor-associated protein |   |  |
| CC  | (HRAP) from Incyte clone 3083742 obtained from OVARFUN01 cDNA library.    |   |  |
| CC  | This sequence is expressed in haematopoietic/immune, gastrointestinal and |   |  |
| CC  | reproductive tissues. HRAP has cytostatic, immunomodulatory,              |   |  |
| CC  | antiinflammatory, cardiant, antiarteriosclerotic, hepatotropic,           |   |  |
| CC  | antiarthritic, antirheumatic, osteopathic, antiallergic, antianaemic,     |   |  |
| CC  | antiasthmatic, antidiabetic, dermatological and neuroprotective           |   |  |
| CC  | activities. The present sequence is useful in the diagnosis, treatment    |   |  |
| CC  | and prevention of disorders associated with HRAP expression, especially   |   |  |
| CC  | cell proliferative, autoimmune/inflammatory, reproductive, cardiovascular |   |  |
| CC  | and gastrointestinal disorders (e.g. atherosclerosis, cirrhosis,          |   |  |
| CC  | leukemia, cancer, AIDS, arthritis, allergies, anaemia, asthma,            |   |  |
| CC  | dermatitis, diabetes, osteoporosis, multiple sclerosis and irritable      |   |  |
| CC  | bowel syndrome)   |   |  |
| XX  |   |   |  |
| SQ  | Sequence 1369 BP; 245 A; 453 C; 424 G; 247 T; 0 U; 0 Other;               |   |  |
| Query Match 99.1%; Score 922; DB 3; Length 1369;              |   |   |  |
| Best Local Similarity 99.5%; Pred. NO. 8.8e-175;              |   |   |  |
| Matches 925; Conservative 0; Mismatches 15; Indels 0; Gaps 0; |   |   |  |
| QY  | 1 ATGAATGGACCTACACACCTGTGGCTCCAGGACCTACCTGGCCCCCAGGATCAAG 60              |   |  |
| Db  |   |   |  |
| Db  | 45 ATGAATGGACCTACACACCTGTGGCTCCAGGACCTACCTGGCCCCCAGGATCAAG 104            |   |  |
| QY  | 61 CTGGGCTTCTAGCCTACTTGGGCGTCTCTGGTGGCTAGGCTCTCTCTCAACAGCCTG 120          |   |  |
| Db  |   |   |  |
| QY  | 105 CTGGGCTTCTAGCCTACTTGGGCGTCTCTGGTGGCTAGGCTCTCTCTCAACAGCCTG 164         |   |  |
| Db  |   |   |  |
| QY  | 121 GGGCTCTGGGTGTTCTGCTGCGCATGACAGATGAGACGAGACCCGATCTACATGACC 180         |   |  |
| Db  |   |   |  |
| QY  | 165 GGGCTCTGGGTGTTCTGCTGCGCATGAGCATGAGACGAGACCCGATCTACATGACC 224          |   |  |
| Db  |   |   |  |
| QY  | 181 AACCTGGGCTGGCCGACCTCTGCTGTGTGACACTTTCCTTCTGTGTGTCACATCCCTG 240        |   |  |
| Db  |   |   |  |
| QY  | 225 AACCTGGGCTGGCCGACCTCTGCTGTGTGACACTTTCCTTCTGTGTGTCACATCCCTG 284        |   |  |
| Db  |   |   |  |
| QY  | 241 CGAGACACTCAGACACCGCGCTGTGCCAGCTCTCCAGGGCATCTACTGACCAACAGG 300         |   |  |
| Db  |   |   |  |
| QY  | 285 CGAGACACTCAGACACCGCGCTGTGCCAGCTCTCCAGGGCATCTACTGACCAACAGG 344         |   |  |
| Db  |   |   |  |
| QY  | 301 TACATGAGCATCAGCCTGTGTCACGGCCATCGCGGTGACCGCTATGTGGCGTGGGCAC 360        |   |  |
| Db  |   |   |  |
| QY  | 345 TACATGAGCATCAGCCTGTGTCACGGCCATCGCGGTGACCGCTATGTGGCGTGGGCAC 404        |   |  |
| Db  |   |   |  |
| QY  | 361 CGCTGCGTGGCCGCGGCTGCGTCTCCCCAGGCGAGGCTGCGCGCGTGTGCGCGTCTTC 420        |   |  |
| Db  |   |   |  |
| QY  | 405 CGCTGCGTGGCCGCGGCTGCGTCTCCCCAGGCGAGGCTGCGCGCGTGTGCGCGTCTTC 464        |   |  |
| Db  |   |   |  |
| QY  | 421 TGGGTGCTGCTCATCGGCTCCCTGTGTGCTGTGTGCTGTGTGCTGTGTGCTGTGTGCT 480        |   |  |
| Db  |   |   |  |
| QY  | 465 TGGGTGCTGCTCATCGGCTCCCTGTGTGCTGTGTGCTGTGTGCTGTGTGCTGTGTGCT 524        |   |  |
| Db  |   |   |  |
| QY  | 481 TTCTGCTTCAGGAGCACCGGCAAAATTTCAATGCCATGCCGTTCCCGCTGCTGGATTC 540        |   |  |
| Db  |   |   |  |
| QY  | 525 TTCTGCTTCAGGAGCACCGGCAAAATTTCAATGCCATGCCGTTCCCGCTGCTGGATTC 584        |   |  |
| Db  |   |   |  |
| QY  | 541 TACCTGCCCTTGGCGCTGTGTGCTCTTCTGCTCCCTGAAAGTGTGTGCTGCTGCCCTG 600        |   |  |
| Db  |   |   |  |
| QY  | 585 TACCTGCCCTTGGCGCTGTGTGCTCTTCTGCTCCCTGAAAGTGTGTGCTGCTGCCCTG 644        |   |  |
| Db  |   |   |  |
| QY  | 601 AGGCCACCCACCGACGTGGGCGAGGACAGGACCCCGAGGCTAAAGCATGTGTCTGG 660          |   |  |
| Db  |   |   |  |
| QY  | 645 AGGCCACCCACCGACGTGGGCGAGGACAGGACCCCGAGGCTGCGCGCATGTGTCTGG 704         |   |  |
| Db  |   |   |  |
| QY  | 661 GCCAACCTCTCTGCTGTGTGCTGTGTGCTGTGTGCTGTGTGCTGTGTGCTGTGTGCT 720         |   |  |
| Db  |   |   |  |
| QY  | 705 GCCAACCTCTCTGCTGTGTGCTGTGTGCTGTGTGCTGTGTGCTGTGTGCTGTGTGCT 764         |   |  |
| Db  |   |   |  |
| QY  | 721 CTGCGAGTGGGCTGGAACGCTCTGTGCTCTCTGAGAGCATCCGTCGCGCCCTGTACATA 780       |   |  |
| Db  |   |   |  |
| QY  | 765 CTGCGAGTGGGCTGGAACGCTCTGTGCTCTCTGAGAGCATCCGTCGCGCCCTGTACATA 824       |   |  |
| Db  |   |   |  |
| QY  | 781 ACCAGCAAGCTCTCAGATGCCAATCTGCTGCTGGAGCGCATCTGCTACTACTACATGGCC 840      |   |  |
| Db  |   |   |  |
| QY  | 825 ACCAGCAAGCTCTCAGATGCCAATCTGCTGCTGGAGCGCATCTGCTACTACTACATGGCC 884      |   |  |
| Db  |   |   |  |
| QY  | 841 AAGGAGTTCCAGAGGCGCTGTGACCTGCGCGTGGCTCCCGTGTAAAGCCCAAAAGC 900          |   |  |
| Db  |   |   |  |
| QY  | 895 AAGGAGTTCCAGAGGCGCTGTGACCTGCGCGTGGCTCCCGTGTAAAGCCCAAAAGC 930          |   |  |
| Db  |   |   |  |
| QY  | 901 CAGGACTCTCTGTGCTGACCCCTCGCCCTAA 930                                   |   |  |
| Db  |   |   |  |
| QY  | 945 CAGGACTCTCTGTGCTGACCCCTCGCCCTAA 974                                   |   |  |
| Db  |   |   |  |
| RESULT 9  |   |   |  |
| AAA27485  |   |   |  |
| ID  | AAA27485 standard; cDNA; 1875 BP.   |   |  |
| XX  | AAZ27485;   |   |  |
| AC  | AAZ27485;   |   |  |
| XX  | 15-AUG-2000 (first entry)   |   |  |
| DT  | Human G protein coupled receptor GPR35 gene.                              |   |  |
| XX  |   |   |  |
| XX  | GPR35; G protein coupled receptor; human; NIDDM1;                         |   |  |

non-insulin-dependent diabetes mellitus; CAPN10 gene; calpain 10; diagnosis; therapy; ss.

**Homo sapiens.**

| Key | Location/Qualifiers |
|-----|---------------------|
| CDS | 576..1505           |
|     | /*tag= a            |
|     | /transl_except= (po |
|     | /transl_except= (po |

WO200023603-A2.

27-APR-2000.

21-OCT-1999; 99WO-US024890.

21-OCT-1998: 98US-0105052P.

21-001-1999;  
13-MAY-1999;  
99US-0134175P.

(ARCH-) ARCH DEV CORP.  
(TEXA ) UNIV OF TEXAS SYSTEM.

Polonsky KS, Horikawa Y, Oda N, Sreenan S, Zhou Y, Otani K;

Handis CL, Bell GI, Cox NJ

**WPI: 2000-339702/29.**

P-PSDB: AAY79576, AAY79574, AAY79576.

Method for screening for type 2 diabetes mellitus comprises detecting a polymorphism in a calpain encoding nucleic acid segment or a protease-encoding nucleic acid segment.

Claim 74: page 238: 257pp: English.

The present sequence corresponds to a transcript of the human gene encoding G protein coupled receptor GPR35 (see AAY9576). The sequence of GPR35 is similar to that of a putative purinoceptor P2Y9 (34.1% identity) suggesting that ATP or other nucleotide is its ligand. GPR35 mRNA was detected in all adult and foetal tissues examined with relatively higher levels in adult lung, small intestine, colon and stomach. In these tissues, there are 2 major transcripts of 2.4 and 4.4 kb, whereas in skeletal muscle there is a single transcript of 9.4 kb. The composite cDNA is 1,875 bp (exclusive of polyA tract) and may lack about 400 bp of the 5' untranslated region. The GPR35 gene was identified in a 49,136 bp region (see ABA22475) located within the NIDDM1 region of human chromosome 2. This region also includes the CAPN10 gene, which encodes a novel calpain-like cysteine protease, designated calpain 10. Mutations in the CAPN10 gene are responsible for susceptibility to type 2 diabetes. Claimed methods for screening for a propensity for type 2 diabetes mellitus are based on detection of a polymorphism in a calpain encoding nucleic acid. Methods are also claimed for identifying modulators of calpain activity, and using these modulators to treat diabetes, in particular through the regulation of an insulin secretory response or insulin mediated glucose transport.

Sequence 1875 BP: 290 A; 593 C; 614 G; 378 T; 0 U; 0 Other;

|                           |        |                     |           |              |
|---------------------------|--------|---------------------|-----------|--------------|
| every Match               | 99.0%; | Score 920.4;        | DB 3;     | Length 1875; |
| 1st Local Similarity      | 99.4%; | Pred. No. 1.9e-174; |           |              |
| Matches 924: Conservative | 0;     | Mismatches 6;       | Indels 0; | Gaps 0;      |

1 ATGATGAGGACCTTACACACCTGTGGCTCCAGCGACTTCACTCTGGSCCCCGACGATCAAG 60  
576 ATGAATGGCACCTTACACACCTGTGGCTCCAGCGACTTCACTCTGGSCCCCGACGATCAAG 635  
61 CTGGGCTTTCACGCTACTTTGGGGGCTCTGCTGGTGTCTAGGCTGTCTGTCAACAGCGCTG 120  
636 CTGGGCTTTCACGCTACTTTGGGGGCTCTGCTGGTGTCTAGGCTGTCTGTCAACAGCGCTG 695  
121 GCGCTCTGGGTGTTTCTGCTGCCCGATGACACAGTGGACGGAGACCGCGATCTCATGAC 180  
696 GCGCTCTGGGTGTTTCTGCTGCCCGATGACACAGTGGACGGAGACCGCGATCTCATGAC 755

XX 30-MAY-2002; 2002WO-18004189.  
XX 30-MAY-2001; 2001US-0293999P.  
PR 22-OCT-2001; 2001US-0330457P.  
PR 19-FEB-2002; 2002US-0357144P.  
XX (BIOM-) BIOMEDICAL CENT.  
XX Baranova AV, Yankovsky NK, Kozlov AP, Lobashev AV, Krukovskaya LL;  
PI WPI; 2003-175241/17.  
XX P-PSDB; ADA84069.  
DR Determining if a nucleic acid is a marker for a phenotype/cell type of  
XX interest, by global comparison of expressed sequence tags known to be  
PT expressed in the phenotype/cell type with all ESTs expressed in normal  
PT tissue.  
XX Claim 23; Page 446-448; 516pp; English.  
XX The invention relates to a novel method for determining if a nucleic acid  
CC is a marker for a predetermined phenotype/cell type of interest from a  
CC biological species. The method comprises performing a global comparison  
CC of a group of expressed sequence tags (ESTs) known to be expressed in the  
CC phenotype/cell type of interest with all ESTs expressed in normal tissue  
CC in order to identify ESTs that are preferentially expressed in the  
CC phenotype/cell of interest. A method of the invention is useful for  
CC determining whether a nucleic acid is a marker for a predetermined  
CC phenotype or cell type of interest from a biological species, preferably  
CC Arabidopsis or human. The cell type of interest is an abnormal cell such  
CC as a tumour cell, and the predetermined phenotype is a stress-induced  
CC phenotype such as hyperosmotic stress or high salt conditions. A method  
CC of the invention is also useful for determining the progression of colon  
CC cancer in a human, for detecting a tumour cell, and for regulating or  
CC preventing the growth of a tumour cell. An antibody of the invention is  
CC useful for detecting the absence or presence of peptides encoded by  
CC tumour-associated markers. A polypeptide of the invention is useful as an  
CC immunogen for vaccinating an animal. The present sequence encodes a  
CC tumour-associated antigen of the invention.  
XX  
SQ Sequence 1875 BP; 290 A; 593 C; 614 G; 378 T; 0 U; 0 Other;  
Query Match 99.0%; Score 920.4; DB 8; Length 1875;  
Best Local Similarity 99.4%; Pred. No. 1.9e-174;  
Matches 924; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
QY 1 ATGAATGGGACCTTACACACCTGTGGCTCCAGGACCTCACCTGGCCCGGCGATCAAG 60  
DB |||||||  
576 ATGAATGGGACCTTACACACCTGTGGCTCCAGGACCTCACCTGGCCCGGCGATCAAG 635  
QY 61 CTGGGCTTCTACCCCTACTTGGGCGTCCCTGCTGGTGTAGGCTGTGCTCAACAGCCGTG 120  
DB |||||||  
636 CTGGGCTTCTACCCCTACTTGGGCGTCCCTGCTGGTGTAGGCTGTGCTCAACAGCCGTG 695  
QY 121 GCGCTCTGGGTGTCTGCTCCGCATGCGAGCAGTGGACCGGACCCGCGATCTACATGACC 180  
DB |||||||  
696 GCGCTCTGGGTGTCTGCTCCGCATGCGAGCAGTGGACCGGACCCGCGATCTACATGACC 755  
QY 181 AACCTGGCGGTGGCGGACCTCTGCTGTGACCTTGGCTTGGCTGACCTCCCTG 240  
DB |||||||  
756 AACCTGGCGGTGGCGGACCTCTGCTGTGACCTTGGCTTGGCTGACCTCCCTG 815  
QY 241 CGAGACACCTCAGACACCGCGCTGTGCCAGCTCTCCGAGGATCTACCTGACCAACAGG 300  
DB |||||||  
816 CGAGACACCTCAGACACCGCGCTGTGCCAGCTCTCCGAGGATCTACCTGACCAACAGG 875  
QY 301 TACATGAGCATCAGCTGTGTCACGGCCATCGCGCTGGAACCGCTATGTGCCGTGGCGCAC 360  
DB |||||||  
876 TACATGAGCATCAGCTGTGTCACGGCCATCGCGCTGGAACCGCTATGTGCCGTGGCGCAC 935  
QY 361 CGGCTGGGTGGCGGCTGGGTGCCCGAGGAGCTGGCGGCTGGGTGGGTGGGTGCTC 420  
DB |||||||

DB 936 CGGCTGGGTGGCGGCTGGGTGCCCGGAGGCTGGCGGCTGGCGGCTGGCGGCTCCTC 995  
QY 421 TGGGTGCTGGTTCATCGGCTCCCTGGTGGCTCCCTGGTGGCTCCCTGGGATTCAGAGAGGCGGC 480  
DB |||||||  
996 TGGGTGCTGGTTCATCGGCTCCCTGGTGGCTCCCTGGTGGCTCCCTGGGATTCAGAGAGGCGGC 1055  
QY 481 TTCTGCTTCAGGAGCACCGGCGACAAATTTCACTCAATGCGGTTCCCGCTGCTGGGATTC 540  
DB |||||||  
1056 TTCTGCTTCAGGAGCACCGGCGACAAATTTCACTCAATGCGGTTCCCGCTGCTGGGATTC 1115  
QY 541 TACCTGCCCCCTGGCGGTGGTGTCTTCTGCTCCCTGAAAGGTGGTGACTGCCCCCTGGCCACAG 600  
DB |||||||  
1116 TACCTGCCCCCTGGCGGTGGTGTCTTCTGCTCCCTGAAAGGTGGTGACTGCCCCCTGGCCACAG 1175  
QY 601 AGGCCACCCACGACGCTGGGCGAGGCGACAGGCGACCCCGAAGGCTTAAACGCAATGCTTGG 660  
DB |||||||  
1176 AGGCCACCCACGACGCTGGGCGAGGCGAGGCGACCCCGAAGGCTTAAACGCAATGCTTGG 1235  
QY 661 GCCAACCTCTGGTGTCTGCTGGTCTGCTTCTGCCCCCTGCAGGTGGGCTGACAGTGGC 720  
DB |||||||  
1236 GCCAACCTCTGGTGTCTGCTGGTCTGCTTCTGCCCCCTGCAGGTGGGCTGACAGTGGC 1295  
QY 721 CTCGAGTGGGCTGAAAGCGCTGCTGCTCCCTGAGAGAGATCCGTCGCGCCCTGTACATA 780  
DB |||||||  
1296 CTCGAGTGGGCTGAAAGCGCTGCTGCTCCCTGAGAGAGATCCGTCGCGCCCTGTACATA 1355  
QY 781 ACCAGCAAGCTCTCAGATGCGCAACTGCTGCTGGAGCGCCATCTGCTACTACTACATGCCC 840  
DB |||||||  
1356 ACCAGCAAGCTCTCAGATGCGCAACTGCTGCTGGAGCGCCATCTGCTACTACTACATGCCC 1415  
QY 841 AAGGAGTTCAGAGGCGCTGCTGCTGCGCGTGGCTCCCGTGTAAAGGCCACAAAAGC 900  
DB |||||||  
1416 AAGGAGTTCAGAGGCGCTGCTGCTGCGCGTGGCTCCCGTGTAAAGGCCACAAAAGC 1475  
QY 901 CAGGACTCTCTGTGCGTGACCTCGCCCTAA 930  
DB |||||||  
1476 CAGGACTCTCTGTGCGTGACCTCGCCCTAA 1505  
RESULT 11  
ADO78086  
ID ADO78086 standard; DNA; 1875 BP.  
XX  
AC ADO78086;  
XX  
DT 26-AUG-2004 (first entry)  
XX  
DE Human GPR35 DNA.  
DE ds; gene; tumour-associated antigen; TAG; cancer; lung cancer;  
KW breast cancer; prostate cancer; colon cancer; stomach cancer;  
KW pancreatic cancer; ear cancer; nose cancer; throat cancer; kidney cancer;  
KW cervical cancer; melanoma; tumour; human; GPR35.  
OS Homo sapiens.  
XX  
PN DE10254601-A1.  
XX  
PD 03-JUN-2004.  
XX  
PF 22-NOV-2002; 2002DE-01054601.  
XX  
PR 22-NOV-2002; 2002DE-01054601.  
XX (GANY-) GANYMED PHARM AG.  
PA  
PI Tuereci O, Sahin U, Koslowski M;  
XX  
DR WPI; 2004-421820/40.  
DR P-PSDB; ADO78094.  
XX  
PT Composition containing inhibitor of expression or activity of specific  
tumor-associated antigens, useful for treating cancers, also related

PT compositions for diagnosis and monitoring.  
 XX Claim 1; SEQ ID NO 1; 124pp; German.  
 XX The invention relates to pharmaceutical compositions that comprise an  
 CC agent that inhibits the expression or activity of a tumour-associated  
 CC antigen (TAG) that is encoded by a nucleic acid. The pharmaceutical  
 CC compositions and related compositions, are used for treatment of diseases  
 CC associated with (abnormal) expression of TAG, specifically cancer e.g. of  
 CC lung, breast, prostate, colon, stomach, pancreas, ear/nose/throat, kidney  
 CC or cervix, also melanoma. Compositions containing TAG, or related nucleic  
 CC acid, antibodies or host cells, are also useful for diagnosis and  
 CC monitoring of tumours. The present sequence represents the human GPR35  
 CC DNA.

XX SQ Sequence 1875 BP; 290 A; 593 C; 614 G; 378 T; 0 U; 0 Other;  
 Query Match 99.0%; Score 920.4; DB 12; Length 1875;  
 Best Local Similarity 99.4%; Pred. No. 1.9e-174;  
 Matches 924; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 ATGAATGGCACTTACCAACACCTGTGGCTCCAGGACCTCAGCTGGCCCGCCAGCATCAAG 60  
 Db 576 ATGAATGGCACTTACCAACACCTGTGGCTCCAGGACCTCAGCTGGCCCGCCAGCATCAAG 635  
 Qy 61 CTGGGCTTCTAGCCTACTTGGGCGTCTGCTGGTGTAGGCTGCTGCTCAACAGCCTG 120  
 Db 636 CTGGGCTTCTAGCCTACTTGGGCGTCTGCTGGTGTAGGCTGCTGCTCAACAGCCTG 695  
 Qy 121 CGGCTCTGGGTGTTCTGCTGCGCATGAGCAGATGAGACCGGATCTACATGACC 180  
 Db 696 CGGCTCTGGGTGTTCTGCTGCGCATGAGCAGATGAGACCGGATCTACATGACC 755  
 Qy 181 AACCTGGCGTGGCGGACCTTGCCTGCTGTGCACTTGGCTTGGCTGCACTTCCCTG 240  
 Db 756 AACCTGGCGTGGCGGACCTTGCCTGCTGTGCACTTGGCTTGGCTGCACTTCCCTG 815  
 Qy 241 CGAGACCTCAGACACCGCGTGTGCCAGTCTCCAGGGGATCTACCTGACCAACAGG 300  
 Db 816 CGAGACCTCAGACACCGCGTGTGCCAGTCTCCAGGGGATCTACCTGACCAACAGG 875  
 Qy 301 TACATGACATCAGCTGTGACGCGCATGCGCGTGGACCGTATGTGGCGTGGCGCAC 360  
 Db 876 TACATGACATCAGCTGTGACGCGCATGCGCGTGGACCGTATGTGGCGTGGCGCAC 935  
 Qy 361 CGGCTGCGTGGCGGCGTGGCTTCCCGGAGGCTGGCGCGTGTGGCGGCTCTC 420  
 Db 936 CGGCTGCGTGGCGGCGTGGCTTCCCGGAGGCTGGCGCGTGTGGCGGCTCTC 995  
 Qy 421 TGGGTGCTGCTCATCGGCTCCCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 480  
 Db 996 TGGGTGCTGCTCATCGGCTCCCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1055  
 Qy 481 TTCTGCTTTCAGGACACCGGACAAATTTCACTCCATGCGGTTCCTGCTGGGATTC 540  
 Db 1056 TTCTGCTTTCAGGACACCGGACAAATTTCACTCCATGCGGTTCCTGCTGGGATTC 1115  
 Qy 541 TACCTGCCCCCTGGCGTGGTGTCTTCTGCTCCCTGAAGGTGGTGAATGCTGCCCCAG 600  
 Db 1116 TACCTGCCCCCTGGCGTGGTGTCTTCTGCTCCCTGAAGGTGGTGAATGCTGCCCCAG 1175  
 Qy 601 AGGCCACCCAGCATGTTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 660  
 Db 1176 AGGCCACCCAGCATGTTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1235  
 Qy 661 GCGAACCTCTGCTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720  
 Db 1236 GCGAACCTCTGCTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1295  
 Qy 721 CTCGAGTGGGTGGAACCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780  
 Db 1296 CTCGAGTGGGTGGAACCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1355

Qy 781 ACCAGCAAGCTCTCAGATGCCAACTGTGCTGCGACGCCATCTGCTACTACTATGCGC 840  
 Db 1356 ACCAGCAAGCTCTCAGATGCCAACTGTGCTGCGACGCCATCTGCTACTACTATGCGC 1415  
 Qy 841 AAGGAGTTCAGGAGGCTCTGCACTGCGCGTGGCTCCCGTGGTAAAGGCCCAAAAGC 900  
 Db 1416 AAGGAGTTCAGGAGGCTCTGCACTGCGCGTGGCTCCCGTGGTAAAGGCCCAAAAGC 1475  
 Qy 901 CAGGACTCTCTGTGCTGAGCCCTGCGCTAA 930  
 Db 1476 CAGGACTCTCTGTGCTGAGCCCTGCGCTAA 1505

RESULT 12

AAA27475  
 ID AAA27475 standard; DNA; 49136 BP.  
 XX AC AAA27475;  
 XX AC AAA27475;  
 DT 15-AUG-2000 (first entry)  
 XX NIDDM1 region including CAPN10 and GPR35 genes.  
 XX NIDDM1; non-insulin-dependent diabetes mellitus; CAPN10 gene; calpain 10;  
 KW GPR35 gene; G protein coupled receptor; human; polymorphism; UCSNP-43;  
 KW chromosome 2; diapain-1; diagnosis; therapy; ds.  
 XX Homo sapiens.  
 XX Key Location/Qualifiers  
 FH exon 1235..1515  
 FT /\*tag= a  
 FT /number= 1  
 FT /codon\_start= 1375  
 FT intron 1516..3812  
 FT /\*tag= b  
 FT /number= 1  
 FT exon 3813..3944  
 FT /\*tag= c  
 FT /number= 2  
 FT intron 3945..5282  
 FT /\*tag= d  
 FT /number= 2  
 FT exon 5283..5479  
 FT /\*tag= e  
 FT /number= 3  
 FT exon 5283..5468  
 FT /\*tag= f  
 FT /number= 3\*  
 FT intron 5469..6400  
 FT /\*tag= h  
 FT /number= 3\*  
 FT intron 5480..6400  
 FT /\*tag= g  
 FT /number= 3  
 FT variation replace(6225,a)  
 FT /\*tag= ag  
 FT /frequency= "0.75"  
 FT /note= "G-allele has a frequency of 0.75 in Mexican Americans"  
 FT /frequency= "0.71"  
 FT /note= "G-allele has a frequency of 0.71 in non-Hispanic whites of German ancestry"  
 FT /frequency= "0.90"  
 FT /note= "G-allele has a frequency of 0.90 in African Americans"  
 FT /frequency= "0.94"  
 FT /note= "G-allele has a frequency of 0.94 in Asians (Japanese)"  
 FT 6401..6618  
 FT /\*tag= i  
 FT /number= 4  
 FT intron 6619..8372



```
Db 43825 AACCTGGCGGTGGCCGACCTCTGCTGCTGTGACCTTGCCCTTGCTGCTGCACTCCCTG 43884
Qy 241 CGAGACACCTCAGACACCGCGCTGTGCGAGCTCTCCCGAGGGCATCTACCTGACCAACAGG 300
Db 43885 CGAGACACCTCAGACACCGCGCTGTGCGAGCTCTCCCGAGGGCATCTACCTGACCAACAGG 43944
Qy 301 TACATGAGCATCAGCTTGGTCAACGGCCATCGCCCGTGACCGCTATGTGGCCGTGCGGCAC 360
Db 43945 TACATGAGCATCAGCTTGGTCAACGGCCATCGCCCGTGACCGCTATGTGGCCGTGCGGCAC 44004
Qy 361 CCGCTGGGTGCCCGCGGCTGCGGTCCCGTCCCAAGCAGGCTGCGCGCTGTGGCGGCTCTC 420
Db 44005 CCGCTGGGTGCCCGCGGCTGCGGTCCCGTCCCAAGCAGGCTGCGCGCTGTGGCGGCTCTC 44064
Qy 421 TGGGTGCTGTCATCGGCTCCCTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
Db 44065 TGGGTGCTGTCATCGGCTCCCTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 44124
Qy 481 TTCTGCTTCAGGAGCACCGCGCACAAATTTCAACTCCATGCGGTTCCCGCTGCTGGGATTC 540
Db 44125 TTCTGCTTCAGGAGCACCGCGCACAAATTTCAACTCCATGCGGTTCCCGCTGCTGGGATTC 44184
Qy 541 TACCTGCCCTGGCGGCTGCTGCTCTTCTGCTCCCTGAAAGTGTGTAAGTCCCTGGCCGAG 600
Db 44185 TACCTGCCCTGGCGGCTGCTGCTCTTCTGCTCCCTGAAAGTGTGTAAGTCCCTGGCCGAG 44244
Qy 601 AGGCCACCCACGAGTGGGCGAGGCGACGCGCACCCGCAAGGCTTAAACGATGCTGTGG 660
Db 44245 AGGCCACCCACGAGTGGGCGAGGCGACGCGCACCCGCAAGGCTTAAACGATGCTGTGG 44304
Qy 661 GCCAACCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
Db 44305 GCCAACCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 44364
Qy 721 CTCGAGTGGGTGGAACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
Db 44365 CTCGAGTGGGTGGAACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 44424
Qy 781 ACCAGAAAGCTCTCAGATGCCAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840
Db 44425 ACCAGAAAGCTCTCAGATGCCAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 44484
Qy 841 AAGGAGTTCAGGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900
Db 44485 AAGGAGTTCAGGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 44544
Qy 901 CAGGACTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 930
Db 44545 CAGGACTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 44574
```

## RESULT 13

ADP70563 standard; DNA; 1644 BP.

XX ADP70563;

AC ADF70563;

XX 12-FEB-2004 (first entry)

DT 12-FEB-2004 (first entry)

DE Orphan receptor ligand-related human protein gene SeqID186.

XX ligand; orphan receptor protein; fusion protein; fluorescent protein;  
XX cell expression; green fluorescent protein; GFP; GFP-1; wild-type GFP;  
XX GFPuv; Enhanced GFP; EGFP; human; gene; ds.

OS Homo sapiens.

XX

XX WO2003071272-A1.

XX

XX 28-AUG-2003.

XX

XX 21-FEB-2003; 2003WO-JP001901.

XX

XX

PR 22-FEB-2002; 2002JP-00045728.  
PR 23-JUL-2002; 2002JP-00213949.  
PR 11-OCT-2002; 2002JP-00298237.  
XX  
XX  
XX (TAKE ) TAKEDA CHEM IND LTD.  
XX Hinuma S, Fujii R, Ogi K, Komatsu H, Kawamata Y, Hosoya M;  
XX WPI; 2003-697654/66.  
XX P-PSDB; ADF70461.  
XX  
XX Transformation of cells with a fusion protein of an orphan receptor  
XX protein with a fluorescent protein useful for identification of ligands  
XX to the orphan receptor.  
XX  
XX Example 4; SEQ ID NO 186; 594pp; Japanese.  
XX  
XX This invention relates to a novel method of identifying ligands to an  
XX orphan receptor protein which comprises transforming cells with DNA  
XX encoding a fusion protein of the orphan receptor with a fluorescent  
XX protein, so that the fusion protein is expressed in the cells (or cell  
XX membranes isolated from them) and contacting the cells with the potential  
XX ligand to be tested. A suitable fluorescent protein (GFP), for example GFP-1,  
XX the fusion protein is green fluorescent protein (GFP), for example GFP-1,  
XX wild-type GFP, GFPuv or Enhanced GFP (EGFP). The method is useful for the  
XX identification of ligands binding to an orphan receptor protein.  
XX  
XX Sequence 1644 BP; 368 A; 486 C; 431 G; 359 T; 0 U; 0 Other;

Query Match 98.8%; Score 919; DB 10; Length 1644;

Best Local Similarity 99.5%; Pred. No. 3.6e-174;

Matches 922; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 ATGAATGGCACTACACACCTGTGGCTCCAGGACCTCACCTGGCCCGCCAGCGATCAAG 60  
Db 1 ATGAATGGCACTACACACCTGTGGCTCCAGGACCTCACCTGGCCCGCCAGCGATCAAG 60  
Qy 61 CTGGGCTTCTACGCGCTACTTGGGCGTCTGCTGGTGTAGCGCTGCTCTCAACAGCGTG 120  
Db 61 CTGGGCTTCTACGCGCTACTTGGGCGTCTGCTGGTGTAGCGCTGCTCTCAACAGCGTG 120  
Qy 121 CGGCTCTGGGTGTTCTGCTGCGCATGAGAGCGGAGACCGCATCTACATGACC 180  
Db 121 CGGCTCTGGGTGTTCTGCTGCGCATGAGAGCGGAGACCGCATCTACATGACC 180  
Qy 181 AACCTGGCGGTGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240  
Db 181 AACCTGGCGGTGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240  
Qy 241 CGAGACCTCAGACACCGCGCTGTGCGAGCTCTCCAGGGCATCTACCTGACCAACAGG 300  
Db 241 CGAGACCTCAGACACCGCGCTGTGCGAGCTCTCCAGGGCATCTACCTGACCAACAGG 300  
Qy 301 TACATGAGCATCAGCTTGGTCAACGGCCATGCGCGTGGACCGCTATGTGGCCGTGCGGCAC 360  
Db 301 TACATGAGCATCAGCTTGGTCAACGGCCATGCGCGTGGACCGCTATGTGGCCGTGCGGCAC 360  
Qy 361 CCGCTGCGTGGCGGCGGTGCGGTCGCCAGGAGGCTGCGGCGTGTGCGGCTGCTGCTGCTGCTG 420  
Db 361 CCGCTGCGTGGCGGCGGTGCGGTCGCCAGGAGGCTGCGGCGTGTGCGGCTGCTGCTGCTGCTG 420  
Qy 421 TGGGTGCTGCTCATCGGCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480  
Db 421 TGGGTGCTGCTCATCGGCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480  
Qy 481 TTCTGCTTCAGGAGCACCGCGCACAAATTTCAACTCCATGCGGTTCCCGCTGCTGGGATTC 540  
Db 481 TTCTGCTTCAGGAGCACCGCGCACAAATTTCAACTCCATGCGGTTCCCGCTGCTGGGATTC 540  
Qy 541 TACCTGCCCTGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600  
Db 541 TACCTGCCCTGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600





Qy 841 AAGGAGTTCCAGAGGCGTCTGCACTGGCGTGGCTCCCGTGTAAAGGCCCAAAAGC 900  
 Db |||||  
 Qy 3352 AAGGAGTTCCAGAGGCGTCTGCACTGGCGTGGCTCCCGTGTAAAGGCCCAAAAGC 3411  
 Db |||||  
 Qy 901 CAGGACTCTCTGTGCGTGACCTCGCCTAA 930  
 Db |||||  
 Qy 3412 CAGGACTCTCTGTGCGTGACCTCGCCTAA 3441  
 Db |||||

RESULT 15

AAZ35390  
 ID AAZ35390 standard; cDNA; 1043 BP.

XX AAZ35390;

XX 11-APR-2000 (first entry)

XX Human G-protein coupled receptor GPR35A cDNA.

XX GPR35A; human; G-protein coupled receptor; purinergic;  
 KW 7-transmembrane receptor; antibiotic; antifungal; antiviral; analgesic;  
 KW cytosolic; antidiabetic; anorectic; antiasthmatic; antiparkinsonian;  
 KW hypotensive; hypertensive; osteopathic; antianginal; cardiac;  
 KW cerebroprotective; antiulcer; antiallergic; antimigraine; antiemetic;  
 KW tranquilizer; antidepressant; neuroleptic; nootropic; anticonvulsant;  
 KW gene therapy; diagnosis; vaccine; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

XX CDS 25..954

XX /\*tag= a

XX WO9644452;A1.

XX 16-DEC-1999.

XX 01-JUN-1999; 99WO-US012123.

XX 11-JUN-1999; 98US-00096031.

XX (SMK ) SMITHKLINE BEECHAM CORP.

XX Elshourbagy NA;

XX WPI; 2000-116525/10.

XX P-PSDB; AAY35390.

XX New human GPR35A polypeptides and polynucleotides used to identify

XX agonists, antagonists and inhibitors for use in therapy.

XX Claim 2; Page 32; 38pp; English.

XX The present sequence represents cDNA coding for human GPR35A (see  
 CC AAY58645), a novel member of the purinergic family of polypeptides and a  
 CC G-protein coupled receptor. The invention provides GPR35A polynucleotides  
 CC having at least 70% identity with the present sequence, GPR35A  
 CC polypeptides, recombinant materials, and methods for their production.  
 CC GPR35A polypeptides can be used for identifying agonists and  
 CC antagonists/inhibitors, and for detecting diseases associated with  
 CC inappropriate GPR35A activity or levels. GPR35A polypeptides and  
 CC polynucleotides, agonists, antagonists and antibodies are used to treat:  
 CC infections such as bacterial, fungal, protozoan and viral infections,  
 CC particularly HIV-1 and HIV-2; pain; cancer; diabetes; obesity; anorexia;  
 CC bulimia; asthma; Parkinson's disease; acute heart failure; hypotension;  
 CC hypertension; urinary retention; osteoporosis; angina pectoris;  
 CC myocardial infarction; stroke; ulcers; allergy; benign prostatic  
 CC hyper trophy; migraine; vomiting; psychotic and neurological disorders  
 CC including anxiety, schizophrenia, manic depression, depression, delirium,  
 CC dementia and severe mental retardation; and dyskinesias such as  
 CC Huntington's or Gilles de la Tourette's syndrome. The polynucleotide is  
 CC also useful as a source of primers and probes, and also for detecting the

CC above diseases

XX SQ Sequence 1043 BP; 161 A; 361 C; 315 G; 206 T; 0 U; 0 Other;

Query Match 98.58; Score 915.6; DB 3; Length 1043;  
 Best Local Similarity 99.0%; Pred. No. 1.6e-173; Indels 0; Gaps 0;  
 Matches 921; Conservative 0; Mismatches 9;

Qy 1 ATGAATGGCACCTACAAACACCTGTGGCTCCAGCGACCTACCTGGCCCCCAGCGATCAAG 60  
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 Qy 25 ATGAATGGCACCTACAAACACCTGTGGCTCCAGCGACCTACCTGGCCCCCAGCGATCAAG 84  
 Db |||||  
 Qy 61 CTGGGCTTTACGCTACTTGGGCGTCTGTCTGTGTAGGCTGTCTCAACAGCGCTG 120  
 Db |||||  
 Qy 85 CTGGGCTTTACGCTACTTGGGCGTCTGTCTGTGTAGGCTGTCTCAACAGCGCTG 144  
 Db |||||  
 Qy 121 GCGCTCTGGGTGTTCTGTGCGCATGCAGCAGTGGAGCGAGACCGCATCTACATGACC 180  
 Db |||||  
 Qy 145 GCGCTATGGGTGTTCTGTGCGCATGCAGCAGTGGAGCGAGACCGCATCTACATGACC 204  
 Db |||||  
 Qy 181 AACCTGGCGGTGGCGGACCTCTGCTGTGTGACACCTTTGCCCTTTGCTGTGCTGCTG 240  
 Db |||||  
 Qy 205 AACCTGGCGGTGGCGGACCTCTGCTGTGTGACACCTTTGCCCTTTGCTGTGCTGCTG 264  
 Db |||||  
 Qy 241 CGAGACACCTCAGACACGCGCTGTGCGCTCTCCAGGGGATCTACTGACCAACAGG 300  
 Db |||||  
 Qy 265 CGAGACACCTCAGACACGCGCTGTGCGCTCTCCAGGGGATCTACTGACCAACAGG 324  
 Db |||||  
 Qy 301 TACATGACATCAGCTGTGTCAGGCGCATGCCGTCGTCGTCGTCGTCGTCGTCGTCG 360  
 Db |||||  
 Qy 325 TACATGACATCAGCTGTGTCAGGCGCATGCCGTCGTCGTCGTCGTCGTCGTCGTCG 384  
 Db |||||  
 Qy 361 CCGCTGGCTGCCCGCGGCTGCGGTCCCGCAGGAGGCTGGCGGCGTGTGCGCGTCTCTC 420  
 Db |||||  
 Qy 385 CCGCTGGCTGCCCGCGGCTGCGGTCCCGCAGGAGGCTGGCGGCGTGTGCGCGTCTCTC 444  
 Db |||||  
 Qy 421 TGGGTGCTGTCATGCGCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480  
 Db |||||  
 Qy 445 TGGGTGCTGTCATGCGCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 504  
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 Qy 481 TTCTGCTTCAGAGCACCGGCGACAAATTTCACTCCATCCGCTCCCGCTGCTGGGATTC 540  
 Db |||||  
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 Qy 541 TACCTGCCCCCTGGCGCTGCTGCTTCTGCTCCCTGAAAGTGGTGACTGCTGCTGCTG 600  
 Db |||||  
 Qy 565 TACCTGCCCCCTGGCGCTGCTGCTTCTGCTCCCTGAAAGTGGTGACTGCTGCTGCTG 624  
 Db |||||  
 Qy 601 AGGCCACCCACCGACGTCGGGCGAGCGACGACCGGCGACCGGCGACCGGCGATGTTGG 660  
 Db |||||  
 Qy 625 AGGCCACCCACCGACGTCGGGCGAGCGACGACCGGCGACCGGCGATGTTGGTCTGG 684  
 Db |||||  
 Qy 661 GCCAACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720  
 Db |||||  
 Qy 685 GCCAACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 744  
 Db |||||  
 Qy 721 CTCGAGTGGGCTGGAACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780  
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 Qy 745 CTCGAGTGGGCTGGAACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 804  
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 Qy 781 ACCAGCAGCTCTCAGATGCCAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840  
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 Qy 805 ACCAGCAGCTCTCAGATGCCAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 864  
 Db |||||  
 Qy 841 AAGGAGTTCCAGAGGCGTCTGCACTGGCGTGGCTTCCCGTGTAAAGGCCCAAAAGC 900  
 Db |||||  
 Qy 865 AAGGAGTTCCAGAGGCGTCTGCACTGGCGTGGCTTCCCGTGTAAAGGCCCAAAAGC 924  
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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

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9560.973 Million cell updates/sec

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Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:\*

1: gb\_est1.\*  
2: gb\_est2.\*  
3: gb\_est3.\*  
4: gb\_hcc.\*  
5: gb\_est4.\*  
6: gb\_est5.\*  
7: gb\_est6.\*  
8: gb\_est7.\*  
9: gb\_gss1.\*  
10: gb\_gss2.\*  
11: gb\_gss3.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match % | Length | DB ID       | Description        |
|------------|-------|---------------|--------|-------------|--------------------|
| 1          | 922   | 99.1          | 930    | 10 AY401607 | AY401607 Homo sapi |
| C 2        | 736.4 | 79.2          | 876    | 7 CN834209  | CN834209 AGENCOURT |
| C 3        | 674.2 | 72.5          | 906    | 7 CN835542  | CN835542 AGENCOURT |
| C 4        | 609.8 | 65.6          | 960    | 7 CN843697  | CN843697 AGENCOURT |
| C 5        | 601.2 | 64.6          | 750    | 7 CO921172  | CO921172 AGENCOURT |
| C 6        | 591.2 | 63.6          | 642    | 10 AY401608 | AY401608 Pan trogl |
| C 7        | 581.8 | 62.6          | 778    | 7 CO923163  | CO923163 AGENCOURT |
| C 8        | 571.1 | 61.4          | 759    | 7 CO957219  | CO957219 AGENCOURT |
| C 9        | 549.2 | 59.1          | 924    | 10 AY401609 | AY401609 Mus muscu |
| 10         | 549.2 | 59.1          | 2649   | 4 AK036503  | AK036503 Mus muscu |
| 11         | 544.4 | 58.5          | 3158   | 4 AK034870  | AK034870 Mus muscu |
| 12         | 538.2 | 57.9          | 4254   | 4 AK089198  | AK089198 Mus muscu |
| 13         | 531.2 | 57.1          | 783    | 7 CN835586  | CN835586 AGENCOURT |
| C 14       | 516.6 | 55.5          | 717    | 7 CO923285  | CO923285 AGENCOURT |
| C 15       | 512.6 | 55.1          | 1019   | 7 CN832122  | CN832122 AGENCOURT |
| C 16       | 510.6 | 54.9          | 777    | 7 CO921660  | CO921660 AGENCOURT |
| 17         | 510.4 | 54.9          | 1009   | 2 BB609892  | BB609892 BB609892  |
| 18         | 499.2 | 53.7          | 855    | 7 CN832152  | CN832152 AGENCOURT |
| 19         | 458   | 49.2          | 592    | 3 BM772486  | BM772486 K-EST0056 |
| 20         | 415   | 44.6          | 827    | 7 CN843490  | CN843490 AGENCOURT |
| C 21       | 392.6 | 42.2          | 614    | 9 BZ221309  | BZ221309 CH230-312 |
| 22         | 374.4 | 40.3          | 690    | 5 BY747772  | BY747772 BY747772  |

|      |       |      |     |   |          |                     |
|------|-------|------|-----|---|----------|---------------------|
| 23   | 374.4 | 40.3 | 701 | 5 | BY748928 | BY748928            |
| C 24 | 338.4 | 36.4 | 372 | 2 | BF766676 | BF766676 CM3-CS004  |
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| C 26 | 317.6 | 34.2 | 444 | 1 | AW854188 | AW854188 RC3-CT025  |
| C 27 | 317   | 34.1 | 429 | 1 | AW854178 | AW854178 RC3-CT025  |
| 28   | 317   | 34.1 | 668 | 2 | BB629414 | BB629414 BB629414   |
| 29   | 313.4 | 33.7 | 648 | 7 | CO957232 | CO957232 AGENCOURT  |
| C 30 | 308   | 33.1 | 457 | 1 | AW854180 | AW854180 RC3-CT025  |
| C 31 | 307.4 | 33.1 | 616 | 2 | BF151947 | BF151947 uz22c12.y  |
| C 32 | 307   | 33.0 | 554 | 2 | BE696076 | BE696076 RC3-CT025  |
| C 33 | 305.6 | 32.9 | 351 | 1 | AW854187 | AW854187 RC3-CT025  |
| C 34 | 300.6 | 32.3 | 448 | 1 | AW854198 | AW854198 RC3-CT025  |
| C 35 | 297.4 | 32.0 | 437 | 1 | AW854203 | AW854203 RC3-CT025  |
| C 36 | 296   | 31.8 | 411 | 1 | AW854204 | AW854204 RC3-CT025  |
| C 37 | 296   | 31.8 | 571 | 2 | BE696051 | BE696051 RC3-CT025  |
| C 38 | 293.4 | 31.5 | 459 | 1 | AW854197 | AW854197 RC3-CT025  |
| C 39 | 293.4 | 31.5 | 701 | 6 | CB321988 | CB321988 UI-CF-PN0  |
| C 40 | 293   | 31.5 | 585 | 1 | AW854051 | AW854051 RC3-CT025  |
| C 41 | 290.6 | 31.2 | 368 | 2 | BF764582 | BF764582 CM3-CS004  |
| C 42 | 286.6 | 30.8 | 647 | 7 | CN790753 | CN790753 4125379 B  |
| C 43 | 285.6 | 30.7 | 325 | 2 | BF764700 | BF764700 CM3-CS004  |
| C 44 | 282.8 | 30.4 | 428 | 1 | AW854200 | AW854200 RC3-CT025  |
| C 45 | 278.6 | 30.0 | 581 | 7 | CK975307 | CK975307 4106455 B  |

#### ALIGNMENTS

|                       |  |                     |               |             |                 |
|-----------------------|--|---------------------|---------------|-------------|-----------------|
| RESULT 1              | AY401607   | 930 bp              | DNA           | linear      | GSS 15-DEC-2003 |
| AY401607              | Homo sapiens GPR35 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.  |                     |               |             |                 |
| LOCUS                 | AY401607   |                     |               |             |                 |
| DEFINITION            | AY401607.1 GI:39757596   |                     |               |             |                 |
| ACCESSION             | GSS.   |                     |               |             |                 |
| VERSION               | Homo sapiens (human)   |                     |               |             |                 |
| KEYWORDS              | Homo sapiens   |                     |               |             |                 |
| SOURCE                | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.   |                     |               |             |                 |
| ORGANISM              | 1 (bases 1 to 930)   |                     |               |             |                 |
| REFERENCE             | Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civallo, D.R., Lu, F., Murphy, B., Parriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M. |                     |               |             |                 |
| AUTHORS               | Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios   |                     |               |             |                 |
| TITLE                 | Science 302 (5652), 1960-1963 (2003)   |                     |               |             |                 |
| JOURNAL               | 14671302   |                     |               |             |                 |
| PUBMED                | 2 (bases 1 to 930)   |                     |               |             |                 |
| REFERENCE             | Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civallo, D.R., Lu, F., Murphy, B., Parriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M. |                     |               |             |                 |
| AUTHORS               | Direct Submission  |                     |               |             |                 |
| TITLE                 | Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA  |                     |               |             |                 |
| JOURNAL               | This sequence was made by sequencing genomic exons and ordering them based on alignment.   |                     |               |             |                 |
| COMMENT               | Location/Qualifiers  |                     |               |             |                 |
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| Query Match           | 99.1%  | Score 922;          | DB 10;        | Length 930; |                 |
| Best Local Similarity | 99.5%  | Pred. No. 5.7e-191; |               |             |                 |
| Matches 925;          | Conservative   | 0;                  | Mismatches 5; | Indels 0;   | Gaps 0;         |

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Db 121 GCGCTCTGGGTGTCTGCTGCCCATGCGACAGTGAAGGAGACCCGCACTTACATGACC 180
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DEFINITION CN834209 NIH_MGC_145 Homo sapiens cDNA clone
IMAGE:7001934 3', mRNA sequence.
ACCESSION CN834209
VERSION CN834209.1 GI:47938609
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KEYWORDS  
SOURCE  
ORGANISMEST.  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

1 (bases 1 to 876)  
NIH-MGC <http://mgc.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Daniela S. Gerhard, Ph.D.  
Office of Cancer Genomics  
National Cancer Institute / NIH  
Bldg. 31 Rm10A07 Bethesda, MD 20892  
Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
Tissue Procurement: GPCR Consortium  
cDNA Library Preparation: GPCR Consortium  
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: IRB13 row: a column: 04  
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varies by clone; ORFs were PCR-amplified and cloned into  
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clone and include the following: 5'-EcoRV-XmiI/XhoI-3',  
5'-EcoRV-XmiI/NotI-3', EcoRV (TA cloned, non-directional).  
For information about which gene each clones represents,  
please visit our anonymous ftp site at  
[ftp://image.llnl.gov/image/rearrayed\\_plates/IRB1\\_preSV.dat](http://image.llnl.gov/image/rearrayed_plates/IRB1_preSV.dat)  
a Note: this is a NIH\_MGC Library."

FEATURES  
source

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QY 259 CCGCTGTGTCAGCTCTTCCAGGGCATCTACCTGACCAACAGGTACATGAGCATCAGCTG 318  
Db 667 CCGCTGTGTCAGCTCTTCCAGGGCATCTACCTGACCAACAGGTACATGAGCATCAGCTG 608  
QY 319 GTACAGGCGCATCGCGTGTGACCGCTATGTGGCGGTGGGACCCCGCTGGTGGCCCGGG 378  
Db 607 GTACAGGCGCATCGCGTGTGACCGCTATGTGGCGGTGGGACCCCGCTGGTGGCCCGGG 548  
QY 379 CTGCGGTGCTCCAGGAGGCTGGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 438  
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LOCUS
DEFINITION
AGNCOURT 15864184 NIH MGC 145 Homo sapiens cDNA clone
IMAGE:7001933 3', mRNA sequence.
CN835542
VERSION
EST.
KEYWORDS
SOURCE
Homo sapiens (human)
ORGANISM
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1 (bases 1 to 906)
NIH-MGC http://mgi.nci.nih.gov/
AUTHORS
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
Unpublished (1999)
COMMENT
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: c9apbs-r@mail.nih.gov
Tissue Procurement: GPCR Consortium
cDNA Library Preparation: GPCR Consortium
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: IRB13 row: a column: 03
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QY 180 CAACCTGGCGTGGCGG-ACCTTGTGCTGTGTGCACTTGGCCCTT-CGTGTGCTGCTGCTGCT 237
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D 621 AGGTACATGAGCATCAGCCTGCTCAGCGCCATCCCGCTGAGCCGCTATGTGGCGCTGCGG 562
QY 358 CACCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 417
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ftp://image.llnl.gov/image/rearranged\_plates/IRBI.presv.dat  
a Note: this is a NIH\_MGC Library."

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Db 188 AACCAGCAAGCTCTCAGATGCCAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 129
Qy 840 CAAGAGTTCCAGAGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 899
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DEFINITION Pan troglodytes GPR35 gene, VIRTUAL TRANSCRIPT, partial sequence,  
genomic survey sequence.

ACCESSION AY401608  
VERSION AY401608.1 GI:39757597  
KEYWORDS GSS.

SOURCE Pan troglodytes (chimpanzee)  
ORGANISM Pan troglodytes  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

REFERENCE 1 (bases 1 to 642)  
AUTHORS Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,  
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,  
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,  
Adams,M.D. and Cargill,M.

TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous  
gene trios

JOURNAL Science 302 (5652), 1960-1963 (2003)  
PUBMED 14671302  
REFERENCE 2 (bases 1 to 642)  
AUTHORS Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,  
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,  
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,  
Adams,M.D. and Cargill,M.  
TITLE Direct Submission  
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
Rockville, MD 20850, USA  
COMMENT This sequence was made by sequencing genomic exons and ordering  
them based on alignment.

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Best Local Similarity 93.3%; Pred. No. 1.1e-118;  
Matches 599; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

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Db 1 ATGAATGGCACTACAAATANNNTGTGGCTCCAGTGANNTCANNTGGCCCCCAACATCAAG 60
Qy 61 CTGGGCTTTACGCTTACTTGGGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120
Db 61 CTCGNNNNNNCGCTACTTTGGGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120
Qy 121 GCGCTCTGGGTGTTCTGCTGCCGATGTCAGCAGTGGAGCGAGACCGCATCTATATGACC 180
Db 121 GCGCTCTGGGTGTTCTGCTGCCGATGTCAGCAGTGGAGCGAGACCGNNNNNNCATGACC 180
Qy 181 AACCTGGCGGTGGCGGACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
Db 181 AACCTGGCGGTGGCGGACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
Qy 241 CGAGACACCTCAGACACGCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
Db 241 CGAGACACCTCAGACACGCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
Qy 301 TACATGAGCATCAGCTGTCACGCCATCCCGTGGACCGCTATGTCGCGTGGCGCAC 360
Db 301 TACATGAGCATCAGCTGTCACGCCATCCCGTGGACCGCTATGTCGCGTGGCGCAC 360
Qy 361 CCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
Db 361 CCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
Qy 421 TGGGTGCTGGTTCATGGGCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
Db 421 TGGGTGCTGGTTCATGGGCTCCNNNGTGGCTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
Qy 481 TTCTGCTTCAGAGCACCCGCGCACTTCACTCCATGCGGTTCCCGTGTGCTGCTGCTGCTGCTG 540
Db 481 TTCTGCTTCAGAGCACCCGCGCACTTCACTCCATGCGGTTCCCGTGTGCTGCTGCTGCTGCTG 540
Qy 541 TACCTGCCCCCTGGCGTGGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
Db 541 TACCTGCCCCCTGGCGTGGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
Qy 601 AGGCCACCCACCGAGCTGGGGCAGGACGAGGCCACCCGCAAG 642
Db 601 AGGCCACCCACCGAGCTGGGGCAGGACGAGGCCACCCGCAAG 642
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RESULT 7  
CO923163

| LOCUS                 | 778 bp   | mRNA   | linear    | EST 16-AUG-2004 |
|-----------------------|--|--|-----------|-----------------|
| DEFINITION            | AGNCOCURT_3048658 NIH MGC 145 Homo sapiens cDNA clone  |  |           |                 |
| ACCESSION             | IMAGE:7211810 5', mRNA sequence.   |  |           |                 |
| VERSION               | CO923163   |  |           |                 |
| KEYWORDS              | CO923163.1 GI:51275314   |  |           |                 |
| SOURCE                | EST.   |  |           |                 |
| ORGANISM              | Homo sapiens (human)   |  |           |                 |
| REFERENCE             | Homo sapiens   |  |           |                 |
| AUTHORS               | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  |  |           |                 |
| TITLE                 | Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini;   |  |           |                 |
| JOURNAL               | Hominidae; Homo.   |  |           |                 |
| COMMENT               | 1 (bases 1 to 778)<br>NIH-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a> .<br>National Institutes of Health, Mammalian Gene Collection (MGC)<br>Unpublished (1999)<br>Contact: Daniela S. Gerhard, Ph.D.<br>Office of Cancer Genomics<br>National Cancer Institute / NIH<br>Bldg. 31 Rm10A07 Bethesda, MD 20892<br>Email: <a href="mailto:cgapbs-remail.nih.gov">cgapbs-remail.nih.gov</a><br>Tissue Procurement: GPCR Consortium<br>cDNA Library Preparation: GPCR Consortium<br>cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLML)<br>DNA Sequencing by: Agencourt Bioscience Corporation<br>Clone distribution: MGC clone distribution information can be<br>found through the I.M.A.G.E. Consortium/LLML at:<br><a href="http://image.llnl.gov">http://image.llnl.gov</a><br>Plate: IRB15 row: b column: 12<br>High quality sequence start: 33<br>High quality sequence stop: 640.<br>Location/Qualifiers<br>1..778<br>/organism="Homo sapiens"<br>/mol_type="mRNA"<br>/db_xref="taxon:9606"<br>/clone="IMAGE:7211810"<br>/tissue_type="mixed"<br>/lab_host="DH10B"<br>/clone_lib="NIH_MGC_145"<br>/note="Vector: pCDNA3.1, Site_1: varies by clone; Site_2:<br>varies by clone; ORFs were PCR-amplified and cloned into<br>pCDNA3.1 by the GPCR Consortium. Cloning sites vary by<br>clone and include the following: 5'-EcoRV-XmnI/XhoI-3',<br>5'-EcoRV-XmnI/NotI-3', EcoRV (TA cloned, non-directional).<br>For information about which gene each clone represents,<br>please visit our anonymous ftp site at<br><a href="ftp://image.llnl.gov/image/rearrayed_plates/IRB1.presv.dat">ftp://image.llnl.gov/image/rearrayed_plates/IRB1.presv.dat</a><br>a Note: this is a NIH_MGC Library." |  |           |                 |
| FEATURES              | source   |  |           |                 |
| ORIGIN                |  |  |           |                 |
| Query Match           | 62.6%;   | Score 581.8;   | DB 7;     | Length 778;     |
| Best Local Similarity | 99.5%;   | Pred. No. 1.3e-116;  |           |                 |
| Matches 594;          | Conservative 0;  | Mismatches 2;  | Indels 1; | Gaps 1;         |
| Qy                    | 1  | ATGAATGGCACCTTACAACACCTGTGGGCTCCAGCGACCTCACCTGGCCCCCAGCGATCAAG | 60        |                 |
| Db                    | 34   | ATGAATGGCACCTAC-ACACCTGTGGCTCCAGCGACCTCACCTGGCCCCCAGCGATCAAG   | 92        |                 |
| Qy                    | 61   | CTGGGCTTCTACGGCTACTTGGGGCTCTGTGTGGTGTAGGCTGTGCTCAACAGCCTG      | 120       |                 |
| Db                    | 93   | CTGGGCTTCTACGGCTACTTGGGGCTCTGTGTGGTGTAGGCTGTGCTCAACAGCCTG      | 152       |                 |
| Qy                    | 121  | CGGCTCTGGGTGTTCTGTCGGCATGACAGTGGAGCGGAGCCCGCATCTACATGACC       | 180       |                 |
| Db                    | 153  | CGGCTCTGGGTGTTCTGTCGGCATGACAGTGGAGCGGAGCCCGCATCTACATGACC       | 212       |                 |
| Qy                    | 181  | AACCTGGCGGTGGCGGACCTCTGCTGCTGTGACCTTGGCCCTTGGTGTGCTACCTCCCTG   | 240       |                 |
| Db                    | 213  | AACCTGGCGGTGGCGGACCTCTGCTGCTGTGACCTTGGCCCTTGGTGTGCTACCTCCCTG   | 272       |                 |
| Qy                    | 241  | CGAGACCTTCAGACACGCGCTGTGCGAGCTCTCCAGGGGCATCTACCTGACCAACAGG     | 300       |                 |
| Db                    | 273  | CGAGACCTTCAGACACGCGCTGTGCGAGCTCTCCAGGGGCATCTACCTGACCAACAGG     | 332       |                 |



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Query Match      61.4%; Score 571; DB 7; Length 759;
Best Local Similarity 98.5%; Pred. No. 3e-114;
Matches 607; Conservative 0; Mismatches 6; Indels 3; Gaps 3;

Qy 316 CTGCTCAGCGCCATCGCGGTGACCGCTATGTGCGCGTGGGACACCGCTGCGTGGCCGC 375
Db 635 CTGCTCAGCGCCATCGCGGTGACCGCTATGTGCGCGTGGGACACCGCTGCGTGGCCGC 576

Qy 376 GGGCTGGCGTCCCGCAGGACGCTGCGCGCGTGTGCGCGTCTCTGCGGTGCTGCTCATC 435
Db 575 GGGCTGGCGTCCCGCAGGACGCTGCGCGCGTGTGCGCGTCTCTGCGGTGCTGCTCATC 516

Qy 436 GGGCTCCCTGGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 495
Db 515 GGGCTCCCTGGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 456

Qy 496 ACCCGGACCAATTTCAACTCCATCGGTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 555
Db 455 ACCCGGACCAATTTCAACTCCATCGGTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 396

Qy 556 GTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 614
Db 395 GTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 336

Qy 615 CGTGGGAGGACAGGACGACCGCCAGGCT-AAACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 673
Db 335 CGTGGGAGGACAGGACGACCGCCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 276

Qy 674 TGTTCGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 733
Db 275 TGTTCGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 216

Qy 734 GGAACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 793
Db 215 GGAACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 156

Qy 794 CAGATGCCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 853
Db 155 CAGATGCCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 96

Qy 854 AGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 913
Db 95 AGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 36

Qy 914 CGGTGACCTCGCCTA 929
Db 35 GCG-GACCTCGCCTA 21

RESULT 9
LOCUS AY401609
DEFINITION Mus musculus GPR35 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
ACCESSION AY401609
VERSION AY401609.1 GI:39757598
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 924)
AUTHORS Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
Inferred nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 924)
```

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AUTHORS Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
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Best Local Similarity 77.7%; Pred. No. 1.8e-109;
Matches 704; Conservative 0; Mismatches 193; Indels 9; Gaps 3;

Qy 30 CAGGACCTCAGCTGGCCCCCGGATCAAGCTGGGCTTCTACGCTTCTGGGCGTCT 89
Db 21 CAGCACCTCAGCTGGGCTGCTTCCGTCACAACTTCTTCATCATCTACTCAGCCTTGT 80

Qy 90 GCTGCTAGGCTGCTGCTCAACGCTGGGCTCTGGGTGTTCTGTGCGCATGCA 149
Db 81 GCTGCTGCTGGGCTGCTGCTCAACGCTGGGCTCTGGGTATTCGTATCGATGCA 140

Qy 150 GCAGTGACGAGACCGGCTATACATGACCAACTGCGGTCGCGGCTCTGCTGCT 209
Db 141 CCAGTGACGAGACCGGCTATATATGACCAACTGCTGCTGCGGCTCTGCTGCT 200

Qy 210 GTGCACTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 266
Db 201 CTGCTCTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 260

Qy 267 CCAGCTTCCGAGGCTTACCTGACCAACAGCTATAGCATCAGCTGCTGCTGCTG 326
Db 261 CCAGCTTCCAGGCTTACCTGCGGCAACAGATATAGCATCAGCTGCTGCTGCTG 320

Qy 327 CATCGCTGACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 386
Db 321 CATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 380

Qy 387 CCCAGGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 446
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Qy 447 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 503
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Qy 624 GCGAGAGCCACCGCAAGGCTAAACGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 683
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Qy 684 CTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 743
Db 681 CTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 740

Qy 744 TGCCCTCTGAGAGCATCCGTCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 803
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Db 741 TGCTGCCGAGACACCTTCAGCGTGCCTTCATCCACAGGTAAACTCTCAGACACCAA 800

Qy 804 CTCTGCTGGAGCGCCATCTGCTACTACTACATGCGCAAGGATTCAGGAGCGGTCTGC 863

Db 801 CTCTGCTGGAGCGCCATCTGCTACTACTACATGCGCAGAGATTCAGGAGCGGTCCAA 860

Qy 864 ACTGGCGGTGGCTCCCGTCTTAAGGCCCAAAAGCCAGGACTCTCTGTGGGTGACCT 923

Db 861 GCAGGACAGCTCTTCC---AACACACCCCAAGAGCCAGATTCAGGATTCCTGAGCCT 917

Qy 924 CGCCTA 929

Db 918 CACCTA 923

RESULT 10

AK036503

LOCUS

DEFINITION

AK036503 2649 bp mRNA linear HTC 03-APR-2004

Mus musculus adult male bone cDNA, RIKEN full-length enriched library, clone:9830121M19 product:G protein-coupled receptor 35, full insert sequence.

ACCESSION

AK036503

VERSION

AK036503.1 GI:26331445

KEYWORDS

HTC; CAP trapper.

SOURCE

Mus musculus (house mouse)

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1

Carninci, P. and Hayashizaki, Y.

High-efficiency full-length cDNA cloning

Meth. Enzymol. 303, 19-44 (1999)

10349636

2

Carninci, P., Shibata, Y., Hayata, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.

Normalisation and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes

Genome Res. 10 (10), 1617-1630 (2000)

11042159

3

Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsuina, T., Tashiro, H., Itoh, M., Sumi, N., Iehi, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohata, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.

RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer

Genome Res. 10 (11), 1757-1771 (2000)

11076861

4

The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.

Functional annotation of a full-length mouse cDNA collection

Nature 409, 685-690 (2001)

5

The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

6 (bases 1 to 2649)

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,

Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.

Direct Submission

Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Please visit our web site for further details.

URL:http://genome.gsc.riken.jp/

URL:http://fantom.gsc.riken.jp/.

Location/Qualifiers

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ORIGIN

Query Match 59.1%; Score 549.2; DB 4; Length 2649;

Best Local Similarity 77.7%; Pred. No. 28-109;

Matches 704; Conservative 0; Mismatches 193; Indels 9; Gaps 3;

QY 30 CAGCGACCTTCACCTGCCGCCAGGCTCAAGCTGGGCTTCTACGCTTACTTGGCGCTCT 89

Db 192 CAGCACCTTCAGTGGCGCTGCTTCGCTCAACAACTTCTTACCATTACTCAGCCTGCT 251

QY 90 GCTGGTGTAGGCTGCTGCTCAACAGCGCTGGCGCTGCGGTGTTCTGCTCGCGATGCA 149

Db 252 GCTGGTGTGGCGCTGCTGCTCAACAGCGTGGCCTCTGGGTATTCTGCTATCGCATGCA 311

QY 150 GCAGTGGAGGAGACCGGCATCTACATGACCACTGGCGGTGGCGGACTCTGCTGCTGCT 209

Db 312 CCAGTGGACAGAGACCGGCATCTATATGACCACTGGCGGTGGCGGACTCTGCTGCTGCT 371

QY 210 GTGCACTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 266

Db 372 CTGCTCTTGGCATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 431

QY 267 CCAGCTCTCCAGGGGCTTACTGACCAACAGGTACATGAGCATCAGCTGCTGCTGCTGCT 326

Db 432 CCAGCTCTCAGAGGGCATCTACTCTGGCCAAAGATACATGAGCATGAAGCTTGGTCACTGC 491

QY 327 CATCGCGGTGGACCGCTATGTGGCGTGGCGGACCGCTGCTGCTGCTGCTGCTGCTGCTGCT 386

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Db 492 CATTCGTGTGACCGCTATGTGGAGTGGCGATCCCTCGTGGCGGTGAGCTGCGGTC 551
Qy 387 CCCAGGACAGGCTGCGGCGGTGTGGCGGCTCTCTGGGTGCTGTGTCATCGGCTCCCTGGT 446
Db 552 CCCGAGACAGGCTGACAGTGTGTGGCCCTTTGGGTGATAGTGTGCTACCTCCCTGGT 611
Qy 447 GGCTCGTGTGCTCTGGGATTCAGAGGGGGGCTTCTGCTTCAGGAGC---ACCCGGCA 503
Db 612 AGTGCCTGCGGCTGGGATGTCAGAGGGGTGGCTTCTGCTTCAGAGCAAAACCCGGCG 671
Qy 504 CAATTTCACTCCATGCGGTTCCGCTGCTGGGATTTACTGCGCCCTGGCGGTGGTGGT 563
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Qy 864 ACTGCGCTGCTCCCGTGTGTAAGGCCACCAAGCCAGGACTCTGTCGCTGACCCCT 923
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Qy 924 GGCCTA 929
Db 1089 CACCTA 1094

RESULT 11
AK034870
LOCUS
DEFINITION
Mus musculus 12 days embryo embryonic body between diaphragm region
and neck cDNA, RIKEN full-length enriched library, clone:943005L15
product:G protein-coupled receptor 35, full insert sequence.
ACCESSION
AK034870
VERSION
AK034870.1 GI:26330261
KEYWORDS
HTC; CAP trapper.
SOURCE
Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
1 Carninci, P., Shibata, Y., Hayate, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
11042159
2 Carninci, P., Shibata, Y., Hayate, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
11042159
3 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
Konno, H., Akiyama, J., Nishi, K., Kitsumi, T., Tashiro, H., Itoh, M.,
```

```
TITLE
JOURNAL
PUBMED
REFERENCE
AUTHORS
The RIKEN Genome Exploration Research Group Phase II Team and the
FANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
5 The FANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 3158)
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,
Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,
Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,
Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,
Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,
Koya, S., Kurihara, C., Matsuura, T., Miyazaki, A., Murata, M.,
Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohashi, N.,
Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,
Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,
Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takai-Akahira, S.,
Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
Muramatsu, M. and Hayashizaki, Y.
Direct Submission
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp,
URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
Fax:81-45-503-9216)
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.
Location/Qualifiers
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| Query Match                  |      | 58.5%; Score 544.4; DB 4; Length 3158;                         |      |
| Best Local Similarity        |      | 77.4%; Pred. No. 2.2e-108;                                     |      |
| Matches 701; Conservative    |      | 0; Mismatches 196; Indels 9; Gaps 3;                           |      |
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| QY                           | 90   | GCTGGTCTAGGCTGCTGCTCAACAGCTGGCGCTCTG3GTGTTCTGCTGCGCATGCA       | 149  |
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| QY                           | 387  | CCCAGGACGGCTGCGGCGGTGTGCGCGTCTCTGGGTGCTGCTCATCGCTTCCGTGT       | 446  |
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| QY                           | 447  | GGCTCGCTGCTCTGGGATTCAGAGAGCGGCTTCTGCTTCAGAGC---ACCGGCA         | 503  |
| DB                           | 634  | AGTGCCTGCGCGCTGGGATGAGAGAGGTGGCTTCTCTTCAGAGCAACCCGCGG          | 693  |
| QY                           | 504  | CAATTTCAACTCCATCGGTTCGCGTGTGGGATTTCTACCTGCGCCCTGGCGGTGTGTGT    | 563  |
| DB                           | 694  | CAATTTCAGACCACTGCCTTCTCACTGTGGGATTTCTACCTGCGCGTGGCCATCGTGT     | 753  |
| QY                           | 564  | CTTCTGCTCCCTGAAGGTGTGACTGCTGCGCCAGAGGCGCACCCAGCGTGGGCA         | 623  |
| DB                           | 754  | CTTCTGCTCTTTGCAAGTGTGACTGTGCTATCGAGAGGCGCGCTGATGTGGGCA         | 813  |
| QY                           | 624  | GGCAGAGGCCACCGCAAGCTAAAGCATGTCTTGGGCAACCTCTCTGTTGTGTGTGT       | 683  |
| DB                           | 814  | GGCAGAGGCCACCCAAAGGCCACCCACATGTGTCTGGGCAACTTGGCTGTGTGTGT       | 873  |
| QY                           | 684  | CTGCTTCTGCGCCCTGCATGCTGGGCTGACAGTGGCTCGAGTGGGCTGGAAACGCTGT     | 743  |
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| QY                           | 744  | TGCGCTCTCGAGACGATCCGTGCGCCCTGTACATAAACAGCAAGCTCTCAGATGCCAA     | 803  |
| DB                           | 934  | TGCTGCCCGAGACACCTTCAGCGGTGCCCTGTCCATCACAGGTAAACTCTCAGACCA      | 993  |
| QY                           | 804  | CTGCTGCTGGAGCGCATCTGTCTACTACTATGCGCAAGGATTTCCAGGAGCGTCTGC      | 863  |
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| QY                           | 924  | CGCCTA 929   |      |
| DB                           | 1111 | CACCTA 1116  |      |

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| RESULT 12  | AK089198   |
| LOCUS      |  |
| DEFINITION |  |
| ACCESSION  | AK089198.1 GI:26105132   |
| VERSION    | HTC; CAP trapper.  |
| KEYWORDS   | Mus musculus (house mouse)   |
| SOURCE     | Mus musculus   |
| ORGANISM   | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.   |
| REFERENCE  | 1 Carninci, P. and Hayashizaki, Y.<br>High-efficiency full-length cDNA cloning<br>Meth. Enzymol. 303, 19-44 (1999)<br>10349636   |
| AUTHORS    | 2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.<br>Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes<br>Genome Res. 10 (10), 1617-1630 (2000)<br>11042159  |
| TITLE      | 3 Shibata, K., Itoh, M., Aizawa, K., Nagao, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.<br>RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multipipillary sequencer<br>Genome Res. 10 (11), 1757-1771 (2000)<br>11076861   |
| JOURNAL    | 4 The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.<br>Functional annotation of a full-length mouse cDNA collection<br>Nature 409, 585-590 (2001)   |
| PUBMED     | 5 The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.<br>Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs<br>Nature 420, 563-573 (2002)   |
| REFERENCE  | 6 (bases 1 to 4254)<br>Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sobabe, Y., Tagami, M., Tagawa, A., Takahashi, P., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toyota, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.<br>Direct Submission<br>Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration and Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216) |
| JOURNAL    | TITLE  |
| AUTHORS    | COMMENT  |

Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.  
Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC building Addenbrookes Hospital Cambridge) whose assistance we gratefully acknowledge.  
please visit our web site for further details.  
URL: <http://genome.gsc.riken.jp/>  
URL: <http://fantom.gsc.riken.jp/>.

FEATURES

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Query Match 57.9%; Score 538.2; DB 4; Length 4254;  
Best Local Similarity 77.6%; Pred. No. 5.2e-107; Indels 10; Gaps 4;  
Matches 704; Conservative 0; Mismatches 193;

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| DB | 448  | CAGACCTCAGCTGGCTGCTTCGGTCAACAACCTCTTATCATCTACTCAGCCTTGCT      | 507  |
| QY | 90   | GCTGGTGTAGGCTGCTGTCTCAACAGCTGGCGCTCTGGGTGTCTGTGCCCATGCA       | 149  |
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| QY | 150  | GCAGTGACGAGACCGCATCTACATGACCAACCTGGCGTGGCGCACTCTGCTGCT        | 209  |
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| DB | 628  | CTGCTCTTGCCATTGTGCTGTACTCCTGAAATATAGTCTTCAGACACACCGCTG        | 687  |
| QY | 267  | CCAGCTCTCCAGGGCATCTACCTGACCAACAGGTATATGATGATCAGCTGTGTCAGGC    | 326  |
| DB | 688  | CCAGCTCTCAGGGCATCTACCTGGCCAAACAGATACATGAGCATAGCCTGGTCACTGC    | 747  |
| QY | 327  | CATGCCGTGACCGCTATGTGGCGTGGCGGACCCGCTGCTGCGCGCGGCTGGGTC        | 386  |
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| QY | 387  | CCCCAGGAGCTGGCGCGTGGCGGCTCTCTGGGTGCTGTGTCATCGCTCCCTGGT        | 446  |
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| QY | 504  | CAATTTCATCTCATGCGGTTCCCGCTGCTGGGATCTTACCTGCCCTGGCGGTGGT       | 563  |
| DB | 928  | CAATTTCAGCACCACTGCTCTCTCACTGTGGGATTTACCTGGCGCTGGGCATCGTGGT    | 987  |
| QY | 564  | CTTCTGCTCCCTGAGGTGGTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT     | 623  |
| DB | 988  | CTTCTGCTCTTTCAGAGGTAGTGTGCTATCGAAGAGCGCAGCCGCTGATGTGGGCA      | 1047 |
| QY | 624  | GGCAGAGCCACCCGCAAGGCTAAACGCATGTGTCTGGGCGCAACCTCTCTGCTGGT      | 683  |
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| DB | 1345 | TCACCTA 1351  |      |

RESULT 13

CN835586  
LOCUS  
DEFINITION  
CN835586 783 bp mRNA linear EST 02-JUN-2004  
IMAGE:7001933 5', mRNA sequence.

ACCESSION  
CN835586

VERSION  
CN835586.1 GI:47941241

KEYWORDS  
EST.

SOURCE  
Homo sapiens (human)

ORGANISM

Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.

REFERENCE

1. (bases 1 to 783)  
NIH-MGC <http://mgc.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics

National Cancer Institute / NIH

Bldg. 31 Rm10A07 Bethesda, MD 20892

Email: [cgabs-r@mail.nih.gov](mailto:cgabs-r@mail.nih.gov)

Tissue Procurement: GPCR Consortium

cDNA Library Preparation: GPCR Consortium

cDNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

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High quality sequence stop: 482.

FEATURES

source

1. 783

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/note="Vector: pcDNA3.1; Site 1: varies by clone; Site 2:

varies by clone; ORFs were PCR-amplified and cloned into

pcDNA3.1 by the GPCR Consortium. Cloning sites vary by

clone and include the following: 5'-EcoRV-XmnI/XhoI-3',

5'-EcoRV-XmnI/NotI-3', EcoRV (TA cloned, non-directional).

For information about which gene each clones represents,

please visit our anonymous ftp site at

[ftp://image.llnl.gov/image/rearrayed\\_plates/IRB1.presv.dat](ftp://image.llnl.gov/image/rearrayed_plates/IRB1.presv.dat)

ORIGIN

Query Match 57.1%; Score 531.2; DB 7; Length 783;

Best Local Similarity 94.2%; Pred. No. 1.5e-105;  
Matches 585; Conservative 0; Mismatches 29; Indels 7; Gaps 3;

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QY 61 CTGGGCTTCTACGCTTACTTGGCGTCTGTGGTGTAGGCTGTCTCAACAGCCTG 120
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QY 121 GCGCTCTGGTGTCTGTGGCTGCGCATGACAGCATGAGCGAGACCGCATCTACATGACC 180
Db 129 GCGCTCTGGTGTCTGTGGCTGCGCATGACAGCATGAGCGAGACCGCATCTACATGACC 188
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QY 539 TCTACCTGCTGCTGCGCGGTGTGGTCTTCTGTGCTTCTGTGCTTCTGTGCTTCTGTGCT 593
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RESULT 14

CO923285/c

LOCUS

DEFINITION

IMAGE:7211810 3', mRNA sequence.

CO923285

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

1 (bases 1 to 717)

NIH-MGC http://mgc.ncbi.nlm.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Office of Cancer Genomics

National Cancer Institute / NIH

Bldg. 31 Rm10A07 Bethesda, MD 20892

Email: cgabs-r@mail.nih.gov

Tissue Procurement: GPCR Consortium

CDNA Library Preparation: GPCR Consortium

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov

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High quality sequence stop: 478.

Location/Qualifiers

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/note="Vector: pCDNA3.1; Site 1: varies by clone; Site 2:

varies by clone; ORFs were PCR-amplified and cloned into

pCDNA3.1 by the GPCR Consortium. Cloning sites vary by

clone and include the following: 5'-EcoRV-XmnI/XhoI-3',

5'-EcoRV-XmnI/NotI-3', EcoRV (TA cloned, non-directional).

For information about which gene each clones represents,

please visit our anonymous ftp site at

ftp://image.llnl.gov/image/rearrayed\_plates/IRB1.preSV.dat

a Note: this is a NIH\_MGC Library."

ORIGIN

Query Match

Best Local Similarity 55.5%; Score 516.6; DB 7; Length 717;

Matches 539; Conservative 0; Mismatches 19; Indels 1; Gaps 1;

QY 372 CCGCGGGTGGCTGCGGCGGCTGCGGCGGCTGCGGCGGCTGCGGCGGCTGCGGCTGCGGCT 431

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QY 432 CATCGGCTCCCTGGTGGCTCGCTGCTGCTCGGCGGCTTCAAGAGGCGGCTTCTGCTTCAG 491

Db 537 CATCGGCTCCCTGGTGGCTCGCTGCTGCTCGGCGGCTTCAAGAGGCGGCTTCTGCTTCAG 478

QY 492 GAGCACCGCGCACAAATTTCAACTCAATGCGGTTCCGCTGCTGGGATTTCTACCTGCCCT 551

Db 477 GAGCACCGCGCACAAATTTCAACTCAATGCGGTTCCGCTGCTGGGATTTCTACCTGCCCT 418

QY 552 GCGCGTGGTGTCTCTGCTCCCTGAGGTTGGTGAAGTGGTGAAGTGGTGAAGTGGTGAAGT 611

Db 417 GCGCGTGGTGTCTCTGCTCCCTGAGGTTGGTGAAGTGGTGAAGTGGTGAAGTGGTGAAGT 358

QY 612 CGAGTGGCGCAGCAGAGGCGCACCGCAGGCTAAACGATGGTCTGGGCGCAAGCTCTCT 671

Db 357 CGAGTGGCGCAGCAGAGGCGCACCGCAGGCTAAACGATGGTCTGGGCGCAAGCTCTCT 298

QY 672 GGT 731

Db 297 GGT 238

QY 732 CTGGACCGCTGTGCGCTCTGAGAGCATCGCTGCGGCTGTACATTAACAGCAAGCTCT 791

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QY 792 CTCAGATCCCAACTGTCTGCTGAGCGCATCTGCTACTACTACTACTACTACTACTACTACT 851

Db 177 CTCAGATCCCAACTGTCTGCTGAGCGCATCTGCTACTACTACTACTACTACTACTACTACT 118

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Db 57 GTGGTGAACCTTCGCTTAA 39

RESULT 15

CN832122/c

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GenCore version 5.1.7  
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OM nucleic - nucleic search, using sw model

Run on: February 11, 2006, 04:45:59 ; Search time 213 Seconds  
(without alignments)

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Scoring table: IDENTITY\_NUC  
Gapop 10.0 Gapext 1.0

Searched: 1303057 seqs. 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

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Minimum DB seq length: 0
Maximum DB seq length: 20000000000
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Database : Issued_Patents_NA.*
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2: /cgn2_6/ptodata/1/ina/5 COMB.seq.*
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4: /cgn2_6/ptodata/1/ina/6B COMB.seq.*
5: /cgn2_6/ptodata/1/ina/H COMB.seq.*
6: /cgn2_6/ptodata/1/ina/PCBUS COMB.seq.*
7: /cgn2_6/ptodata/1/ina/PP COMB.seq.*
8: /cgn2_6/ptodata/1/ina/RE COMB.seq.*
9: /cgn2_6/ptodata/1/ina/backfileseq.*
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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query |       | Length | DB                 | ID                  | Description |
|------------|-------|-------|-------|--------|--------------------|---------------------|-------------|
|            |       | Match | %     |        |                    |                     |             |
| 1          | 920.4 | 99.0  | 1875  | 3      | US-09-422-869-21   | Sequence 21, Appl   |             |
| 2          | 920.4 | 99.0  | 49136 | 3      | US-09-422-869-1    | Sequence 1, Appl    |             |
| 3          | 141.8 | 15.2  | 1854  | 3      | US-09-724-864-29   | Sequence 29, Appl   |             |
| 4          | 111.6 | 12.0  | 1098  | 3      | US-09-170-496D-225 | Sequence 225, Appl  |             |
| 5          | 111.2 | 12.0  | 1089  | 3      | US-09-170-496D-3   | Sequence 3, Appl    |             |
| 6          | 111.2 | 12.0  | 1365  | 3      | US-09-016-434-1429 | Sequence 1429, Appl |             |
| 7          | 111.2 | 12.0  | 2693  | 3      | US-09-850-948-1    | Sequence 1, Appl    |             |
| 8          | 110   | 11.8  | 1098  | 3      | US-09-170-496D-117 | Sequence 117, Appl  |             |
| 9          | 110   | 11.8  | 1098  | 3      | US-09-850-948-5    | Sequence 5, Appl    |             |
| 10         | 110   | 11.8  | 1597  | 2      | US-08-724-974A-1   | Sequence 1, Appl    |             |
| 11         | 110   | 11.8  | 1697  | 3      | US-09-364-425B-26  | Sequence 26, Appl   |             |
| 12         | 109.6 | 11.8  | 1089  | 3      | US-09-170-496D-165 | Sequence 165, Appl  |             |
| 13         | 92.6  | 10.0  | 1128  | 3      | US-09-170-496D-193 | Sequence 193, Appl  |             |
| 14         | 91    | 9.8   | 1128  | 3      | US-09-170-496D-201 | Sequence 201, Appl  |             |
| 15         | 91    | 9.8   | 1815  | 3      | US-09-041-545-1    | Sequence 1, Appl    |             |
| 16         | 91    | 9.8   | 1815  | 3      | US-09-327-925-1    | Sequence 1, Appl    |             |
| 17         | 89    | 9.6   | 1167  | 3      | US-09-826-509-574  | Sequence 574, Appl  |             |
| 18         | 89    | 9.6   | 1128  | 3      | US-09-016-434-1446 | Sequence 1446, Appl |             |
| 19         | 87.8  | 9.4   | 1128  | 3      | US-09-071-889-1    | Sequence 1, Appl    |             |
| 20         | 87.8  | 9.4   | 1128  | 3      | US-09-170-068-1    | Sequence 1, Appl    |             |
| 21         | 87.8  | 9.4   | 1128  | 3      | US-09-170-496D-55  | Sequence 55, Appl   |             |
| 22         | 87.8  | 9.4   | 1128  | 3      | US-09-170-496D-69  | Sequence 69, Appl   |             |
| 23         | 87.8  | 9.4   | 2582  | 2      | US-08-480-994-6    | Sequence 6, Appl    |             |
| 24         | 87.8  | 9.4   | 2582  | 2      | US-08-616-844-6    | Sequence 6, Appl    |             |

## ALIGNMENTS

## RESULT 1

```

US-09-422-869-21
; Sequence 21, Application US/09422869
; Patent No. 6235481
; GENERAL INFORMATION:
; APPLICANT: POLONSKY, KENNETH S.
; APPLICANT: HORIKAWA, YUKIO
; APPLICANT: ODA, NAOHISA
; APPLICANT: COX, NANCY J.
; APPLICANT: SHENAN, SEAMUS
; APPLICANT: ZHOU, YUN-PING
; APPLICANT: OTANI, KENICHI
; APPLICANT: HANIS, CRAIG L.
; APPLICANT: BELL, GRAEME I.
; TITLE OF INVENTION: METHODS OF TREATMENT OF TY
; FILE REFERENCE: ARCD:307
; CURRENT APPLICATION NUMBER: US/09/422,869
; CURRENT FILING DATE: 1999-10-21
; EARLIER APPLICATION NUMBER: 60/134,175
; EARLIER FILING DATE: 1999-05-13
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 1875
; TYPE: DNA
; ORGANISM: Human
; US-09-422-869-21

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| Query Match           | 99.0%; | Score   | 920.4;  | DB 3;      | Length | 1875;  |    |      |   |
|-----------------------|--------|---|---------|------------|--------|--------|----|------|---|
| Best Local Similarity | 99.4%; | Prod. No.   | 2e-186; |            |        |        |    |      |   |
| Matches               | 924;   | Conservative  | 0;      | Mismatches | 6;     | Indels | 0; | Gaps | 0 |
| QY                    | 1      | ATGAATGGCACCTCAACACACCTGTGGCTCCAGCAGCACTCACCTGGCCCCCGACGCATCAAG | 60      |            |        |        |    |      |   |
| DB                    | 576    | ATGAATGGCACCTCAACACACCTGTGGCTCCAGCAGCACTCACCTGGCCCCCGACGCATCAAG | 635     |            |        |        |    |      |   |
| QY                    | 61     | CTGGGCTTCTACGCCCTACTTTGGGGCTCTGCTGTGGTCTAGGCTGCTGCTCAACAGCCTG   | 120     |            |        |        |    |      |   |
| DB                    | 636    | CTGGGCTTCTACGCCCTACTTTGGGGCTCTGCTGTGGTCTAGGCTGCTGCTCAACAGCCTG   | 695     |            |        |        |    |      |   |
| QY                    | 121    | CGGCTCTGGGTGTTCTGCTGCCGATGACAGAGTGGACGGAGACCCGCATCTACATGACC     | 180     |            |        |        |    |      |   |
| DB                    | 696    | CGGCTCTGGGTGTTCTGCTGCCGATGACAGAGTGGACGGAGACCCGCATCTACATGACC     | 755     |            |        |        |    |      |   |
| QY                    | 181    | AACCTGGCGGTGGCCGACCTCTGCTGTGTGCACCTTGGCCCTTCGTGCTGCATCCCTG      | 240     |            |        |        |    |      |   |
| DB                    | 756    | AACCTGGCGGTGGCCGACCTCTGCTGTGTGCACCTTGGCCCTTCGTGCTGCATCCCTG      | 815     |            |        |        |    |      |   |



|  |     |  |     |
|--|-----|--|-----|
| QY   | 87  | CTGCTGCTAGGCTGCTCTCAACAGCCTGGCGCTCTGGGTGTTCTGCTGCCGAT        | 144 |
| DB   | 90  | CGTGTGTTGGTGGGCTTCCGGCAACTGCTGTCCCTCTACTTGGCTACTGCGAT        | 149 |
| QY   | 147 | GCACAGTGTGACGAGACCCGCTACTATGACCAACCTGGCGTGGCCGACCTTGCT       | 206 |
| DB   | 150 | CAAGGCCCGAACAAGCTGGGCGTGTACCTGTGCAAACCTGACGGTGGCCGACCTCTTCTA | 209 |
| QY   | 207 | GCTGTGCACTTGGCTTGTGTGCTGCTACCTCCCTGGAGACACCTCAGACAGCCGCTGTG  | 266 |
| DB   | 210 | CATCTGCTGCTGCTGCTTCTGGCTGCACTGCTGTCAGACCACTGCTGCTCA          | 269 |
| QY   | 267 | CCAGCTCTCCAGGGCATCTACCTGACC-----AACAGGTACATGAGCATCAG         | 314 |
| DB   | 270 | CGACCTGTCTCCGAGGTGTGGGCATCTCTCTGTACAGAAACATCTATACAGCGTGGG    | 329 |
| QY   | 315 | CCTGGTCAACGGCCATCCCGCTGGACCGCTATGTGGCGCTGGGCAACCGCTGCGGCCG   | 374 |
| DB   | 330 | CTTCTCTGTGCTGCTCTCCGTGGACCGCTACCTGGCTGTGGCCATCCCTTCGCTTCCA   | 389 |
| QY   | 375 | CGGCTCGGTCCTCCCAAGCAGGCTGCGGCCGCTGTGCGCGTCTCTTGG-----T       | 425 |
| DB   | 390 | CCAGTTCGGACCCCTGAAGCGCGCGCTCGGCGTCAGCGTGTCTCTGGCCCAAGGAGCT   | 449 |
| QY   | 426 | GCTGGTCACTGGCTCCCTGGTGGCTCGCTGGCTCCTGGGATTCAGGAGGGCGGCTCTG   | 485 |
| DB   | 450 | GCTGACAGCATCTACTCTCTGATGTCAGAGGAGGTCAATCAGGACGAGAACCGACACG   | 509 |
| QY   | 486 | CTTCAGGAGCAACCGGCAACATTTCACTCCATCGGTTCCCGCTGCTGGGATTTCTACCT  | 545 |
| DB   | 510 | CGTGTCTTTGAGCACTACCCATCCAGGCATGGCAGCGCGCATCACTACTACGCTT      | 569 |
| QY   | 546 | GCCCTCGCCGTGGTGGTCTTCTGCTCCCTGAAGTGTGACTGCCCTGGCCCGAGAGCC    | 605 |
| DB   | 570 | CCTGGTGGCTTCTCTTCCCATCTGCTCTGTGCGCTCCTACGAGGCATCTCTGG        | 629 |
| QY   | 606 | ACCC-----ACCGAGTGGGGCAGCAGACGCCACCGCAAGGCTAAACGCATGCT        | 656 |
| DB   | 630 | CGCCGTGCGCGAGGCCACCGCACCCCAAGAGCGCGCAAGGACCAAGTCAACGCGCTGT   | 689 |
| QY   | 657 | CTGGGCCAACCTCTCTGGTGTTCGTGCTCTGCTTCTGCCCTGCACTGGGCTGACAGT    | 716 |
| DB   | 690 | GCTCAGACCGTGGTCACTCTCTGGCCCTGCTTCTGCGCTACCACTGTTGCTGTGTT     | 749 |
| QY   | 717 | GCGCTCGCAGTGGGCTGGAAACGCTGTGCCCTCTCGGAGACGATCCGTCGGCCCTGTA   | 776 |
| DB   | 750 | GCGCAGC---GTCGGAGGCCAGCTGCGACTTCTGCCAAGGCGGTTTTCAACGCTACCA   | 806 |
| QY   | 777 | CATAACGAGCAAGCTCTCAGATGCCAACTGTGCTCGACGCGCATCTGCTACTACTACAT  | 836 |
| DB   | 807 | CTTCTCCCTCTGCTCACAGCTTCAACTGGGTGCGCGACCCCGTCTCTACTGCTTCTG    | 866 |
| QY   | 837 | GGCCAAGAGTTCACGAGG 856                                       |     |
| DB   | 867 | CAGCGAGACCAACCCACCGG 886                                     |     |
| RESULT 5   |     |  |     |
| US-09-170-496D-3   |     |  |     |
| ; Sequence 3, Application US/09170496D                                       |     |  |     |
| ; Patent No. 6555339   |     |  |     |
| ; GENERAL INFORMATION:   |     |  |     |
| ; APPLICANT: Behan, Dominic P.   |     |  |     |
| ; APPLICANT: Chalmers, Derek T.  |     |  |     |
| ; APPLICANT: Liaw, Chen W.   |     |  |     |
| ; TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human |     |  |     |
| ; TITLE OF INVENTION: Receptors  |     |  |     |
| ; FILE REFERENCE: AREN-0040  |     |  |     |
| ; CURRENT APPLICATION NUMBER: US/09/170,496D                                 |     |  |     |
| ; NUMBER OF SEQ ID NOS: 294  |     |  |     |
| ; CURRENT FILING DATE: 1998-10-13  |     |  |     |
| ; SOFTWARE: PatentIn version 3.1   |     |  |     |
| ; SEQ ID NO 3  |     |  |     |

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; LENGTH: 1089
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-170-496D-3

Query Match      12.0%; Score 111.2; DB 3; Length 1089;
Best Local Similarity 50.3%; Pred. No. 1.4e-14;
Matches 309; Conservative 0; Mismatches 293; Indels 12; Gaps 1;

QY 98 TAGGCTGTGCTCAACAGCTGGCGCTCTGGGTGTTCTGCTGCCGATCAGCAGTGA 157
Db TGGGGCTGCCCAACTGCTGGCTCTGTGGGGCTTACCGCAGGTGCAACAGGCA 148

QY 158 CGAGAGCCGCTATACATGACCAACTGGGGTGGCGGCTCTGCTGCTGCTGACCT 217
Db ACAGAGTGGGCTTACCTGATGAACCTCAGCATCGCGGCTCTGTATATGTCACGC 208

QY 218 TGCCCTTGGTGTGCTCACTCCCTCGAGAC-----ACCTCAGACAGCGCGTGT 265
Db TGGCGTGTGGGTGGACTTCTGTGACACAGCAACTGGATCCAGGCGCGCGGTCT 268

QY 266 GCAGCTCTCCAGGGCATCTACTGACCAAGGTATACATGAGCATCAGCTGGTCA 325
Db GCAAGCTCTTGGGTTCATCTTACACCAATATCTACATCAGCATGCGCTTCTGTGCT 328

QY 326 CATGCGCTGGAGCCGTATGTGGCGGTGGCGGCAACCGCTGCGTGGCGGGCTGGGT 385
Db GCATCTGGGTGGACCGCTACTGGCTGTGGCCACCCCACTCCGCTTGGCCGCGCTGGCC 388

QY 386 CCCCAGGAGGCTGGCGCGTGGCGGCTCTCTGGGTGCTGCTCATCGGCTCCCTGG 445
Db GCGTCAAGACCGCGTGGCGGTGAGCTTCGCTGTGGTGTGGGCGCAGAGCTGGGCGCACT 448

QY 446 TGCTCGTGGCTCTCTGGGGAATTCAGAGGCGGCTTCTGCTTCAGAGACACCGGCA 505
Db CGGCGCGCTTCCATGACGAGCTCTTCCGAGACCGCTACACCACTTCTGTGTTG 508

QY 506 ATTTCATCTCATGCGGTTCGCGTGTGGGATTTACTTGGCGCTGGCGGTGGGTCT 565
Db AGAAGTTCCCATGGAAGGTGGGTGGCTTGGATGAACCTCTATCGGGTGTTCGTGGGT 568

QY 566 TCTGCTCCCTGAAGGTGGTACTGCTGCGTGGCGGCGGCGGCGGCGGCGGCGG 625
Db TCTCTTCCGTGGCGCTCATGCTGCTGTGTCAGCGGGCATCTTGGCGGCGGTGGGG 628

QY 626 CAGAGGCCACCGCAAGGCTAAACGATGCTTCTGGGCGCACTCTCTGGTGTCT 685
Db GCAGCGTGTCCACCGAGCGCCAGGAGAGGCAAGATCAAGCGGCTGGCGCTCAGCCTCA 688

QY 686 GCTTCTGCGCGCTG 699
Db TCGCCATCGTGTGCTG 702

RESULT 6
US-09-016-434-1429
; Sequence 1429, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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QY 686 GCTTCCTGCCCTG 699  
Db 905 TCGCATCGTCTG 918

## RESULT 7

US-09-850-948-1  
; Sequence 1, Application US/09850948  
; Patent No. 6919176  
; GENERAL INFORMATION:  
; APPLICANT: Yang, Jianxin  
; APPLICANT: An, Songzhu  
; APPLICANT: Tularik Inc.  
; TITLE OF INVENTION: Polypeptides and Nucleic Acids Associated With Cancer  
; FILE REFERENCE: 019781-008300US  
; CURRENT APPLICATION NUMBER: US/09/850,948  
; CURRENT FILING DATE: 2001-05-07  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 2693  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: human G-protein coupled receptor 4 (GPR4)  
; NAME/KEY: CDS  
; LOCATION: (594)..(1682)  
; OTHER INFORMATION: human G-protein coupled receptor 4 (GPR4)  
US-09-850-948-1

Query Match 12.0%; Score 111.2; DB 3; Length 2693;  
Best Local Similarity 50.3%; Pred. No. 1.6e-14;  
Matches 309; Conservative 0; Mismatches 293; Indels 12; Gaps 1;  
QY 98 TAGGCTGTCTCAACAGCTGGCGCTCTGGTGTCTTCTGTCGCCGATGAGCAGTGGGA 157  
Db 682 TGGGGTGGCCACCACTGCTGCTCTGGCGGCTTACCGCAGGTGCACAGCGCA 741  
QY 158 CGAGACCGCATATACATGACCAACCTGGGGTGGCGACCTTGTGCTGTGTCACCT 217  
Db 742 ACGAGCTGGCGCTTACCTGATGAACCTCAGCATCGCGACCTGTGTACATCTGACGC 801  
QY 218 TGGCTGTGTGCTGCTCTCTGCGAGC-----ACCTCAGCAGCGCGTGT 265  
Db 802 TGGCGCTGTGGTGAATCTCTTGTGACCAAGCACTGATTCACGGCGCGGCTCT 861  
QY 266 GCCAGCTCTCCAGGCGATCTACCTGACCAAGGTATACATGAGCATGAGCTGTGTCAGG 325  
Db 862 GCAAGCTCTTGGGTTCATCTTCTACACCAATATCTACATCAGCATCGCTTCTGTGCT 921  
QY 326 CCATCGCGTGGACCGCTATGTGGCGGTGGCGACCGCGTGGCGCGCGGCTGCGGT 385  
Db 922 GCATCTCGGTGACCGCTACCTGGTGTGGCGGCGACCACTCGCTTGGCGCGCGGCT 981  
QY 386 CCCCAGGAGCGGTGGCGCGGTGTGGCGGTCTCTGTGGTGTGTGTCATCGGCTCCCTGG 445  
Db 982 GCGTCAAGACCGCGGTGGCGGTGAGCTCGGTGTGGCGGCGCGAGCTGGGCGCGCACT 1041  
QY 446 TGGCTGTGCTCTCTGGGATTCAGGAGGCGGCTTCTGTCTCAGGAGCACCGCGACA 505  
Db 1042 CGGCGCGCTGTTCATGATGAGAGCTTCTCGAGACCGCTTACACCACTTCTGTGTTG 1101  
QY 506 ATTTCAACTCCATGCGGTTCGCGTCTGGGATTTCTACCTGCCCTTGGCGGTGGTCT 565  
Db 1102 AGAAGTTCCCATGGAAGGCTGGGTGGCTGGATGAACCTCTATCGGGTTCGTGGGT 1161  
QY 566 TCTGCTCTGAAGGTGGTGAATGCTGCTGCGCGCGAGAGGCCACCCAGCAGTGGGCGAG 625  
Db 1162 TCTCTTCCGCTGGGCGCTCATGCTGTCTGTACCGGGGCGATCTCTCGGCGCGGTGCGGG 1221  
QY 626 CAGAGGCCACCGCAGGCTTAACGATGCTCTGGGCGCAACTCTCTGTGGTCTGCTGTCT 685

Db 1222 GCAGCGTGTCCACGAGCGCCAGGAGAACAGATCAAGCGGCTGGCCCTCAGCCTCA 1281  
QY 686 GCTTCCTGCCCTG 699  
Db 1282 TCGCATCGTCTG 1295

## RESULT 8

US-09-170-496D-117  
; Sequence 117, Application US/09170496D  
; Patent No. 6555339  
; GENERAL INFORMATION:  
; APPLICANT: Behan, Dominic P.  
; APPLICANT: Chalmers, Derek T.  
; APPLICANT: Liaw, Chen W.  
; TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein-  
; TITLE OF INVENTION: Receptors  
; FILE REFERENCE: AREN-0040  
; CURRENT APPLICATION NUMBER: US/09/170,496D  
; CURRENT FILING DATE: 1998-10-13  
; NUMBER OF SEQ ID NOS: 294  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 117  
; LENGTH: 1098  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-170-496D-117

Query Match 11.8%; Score 110; DB 3; Length 1098;  
Best Local Similarity 50.2%; Pred. No. 2.4e-14;  
Matches 402; Conservative 0; Mismatches 365; Indels 33; Gaps 4;  
QY 87 CCTGCTGTGTAGCGCTGTGCTCAACAGCTGGCGCTCTGGGTGTCTGTGTCGCGCAT 146  
Db 90 CGTGTGTGTGTGGCTTCCGCGCAACTGCTGTCTCTACTTGGCTACTGTCAGAT 149  
QY 147 GCAGCAGTGGACGAGACCCGCATCTACATGACCAACTGCGGTGGCGGACCTTGTGCT 206  
Db 150 CAAGCCCGAAGCAGCTGGCGGTACTGTGCAACTGACGCTGGCGGCGACCTCTTCTA 209  
QY 207 GCTGTGACCTTGGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 266  
Db 210 CATCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 269  
QY 267 CCAGCTCTCCAGGCGCATCTACTGACC-----AACAGGTATACATGAGCATCAG 314  
Db 270 GCAGCTGTCTGCGCAGGTGTGGGCTCTCTGTACGAGAACATCTACATCAGCGTGG 329  
QY 315 CTTGTACAGGCGCATTCGCGTGGACCGCTATGTGGCGGTGGCGCACCGCTGCTGCGCG 374  
Db 330 CTTCCTCTGTGCTGCTCTCGGTGGACCGCTACTGCTGTGGCGCATCCCTTCCGCTTCCA 389  
QY 375 CGGGCTGCGGTCTCCCGAGGAGGTGGCGGTGTGGCGGTGTGGCGGTCTCTGCGG-----T 425  
Db 390 CCAGTTCCGACCCCTGGAAGGCGCGCTGCGGCTCAGCGTGTGCTCTGCGGCAAGAGCT 449  
QY 426 GCTGTGCTATCGGCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 485  
Db 450 GCTTACCGAGCATCTACTTCTCTGATGACGAGAGGTCTATCGAGGAGAGAACAGCAGCG 509  
QY 486 CTTACAGGAGCACCCCGGCAAAATTTCAACTTCCATGCGGTTCGCGCTGCTGGGATTTTACT 545  
Db 510 CGTGTCTTTGAGCATACCCCATCCAGGATGCGAGCGCGCATCAACTACTACCGCTT 569  
QY 546 GCCCTTGGCGGTGTGCTTCTGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 605  
Db 570 CTTGTGTGCTTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 629  
QY 606 ACC-----ACCGAGGTGGGCGAGCAGAGGCCACCCCGCAAGGCTTAACGATGCT 656  
Db 630 CGCGCTGCGCGGAGCCACCGCACCCGCAAGAGCGCGCAGGACCATCATCAGCGGTGT 689  
QY 657 CTGGGCGCAACTCTCTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 716



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Query Match      11.8%; Score 110; DB 2; Length 1597;
Best Local Similarity 50.2%; Pred. No. 2.6e-14;
Matches 402; Conservative 0; Mismatches 365; Indels 33; Gaps 4;

QY 87 CCTGCTGCTGCTAGGCTGCTGCTCAACAGAGCTGGCGCTCTGGGTGTTCTGCTGCCGAT 146
DB 431 CGTCTGGTGGGCTTCCGGCCAACTGCTGCTCTCTACTTCCGCTACCTGCGAT 490
QY 147 GCAGAGTGGACGAGAGCCCGCATCTCATGACCACTTGGCGGTGGCGGACCTTGGCT 206
DB 491 CAAGCCCGGAAACAGAGCTGGCGGTGCTGCTGCAACCTGACGGTGGCGGACCTTCTTA 550
QY 207 GCTGTGACCTTCCCTTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 266
DB 551 CATCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 610
QY 267 CCAGCTCTCCAGGCGCATCTACCTGACC-----AACAGGTACATGAGCATCAG 314
DB 611 CGACTGTCTGCCAGGTGTGGGATCTCTCTGTACGAGAATCTATACATCAGGTGG 670
QY 315 CCTGCTACGCGCATTCGCTGGAGCGCTATGCTGGCGGTGGCGGACCGCTGGTGGCG 374
DB 671 CTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 730
QY 375 CGGCTGGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 425
DB 731 CCAGTTCGCGACCTTGAAGGCGCGCTGCGGCTGAGCTGTGCTGCTGCTGCTGCTGCT 790
QY 426 GCTGTGATCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 485
DB 791 GCTGACAGCATCTACTTCTGATGCAAGAGAGTCTATCGAGGACGAGAACAGCACCG 850
QY 486 CTTGAGGAGCACCGCGCAAAATTTCAACTCCATGCGGTTCGCGTGTGGGATTTACT 545
DB 851 CGTGTGCTTTGAGCATCTACCCCATCCAGCATGGCAGCGCGCATCAACTACTACCGCT 910
QY 546 GCCCTGCGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 605
DB 911 CTTGCTGGGCTTCTCTTCTTCCCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 970
QY 606 ACCC-----ACCGAGCTGGGCGAGGAGGCGCCAGGCTAAACGCGATGCT 656
DB 971 CGCGTGGCGCGGAGCCAGCGCACCCAGAGAGCCGAGAGAGCCAGAGTCCAGCGCTG 1030
QY 657 CTGGGCAACCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 716
DB 1031 GCTGAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1090
QY 717 GCGCTCGAGTGGGCTGGAACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 776
DB 1091 GCGCAGC---GTCTGGAGGCGAGCTGCGACTTCCGCAAGGCGCTTTCAACGCGCTACCA 1147
QY 777 CATACACGAGCTCTCAGATGCCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 836
DB 1148 CTCTCTCTCTCTGCTCAGAGCTTCAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1207
QY 837 GCGCAAGGATTTCCAGGAGG 856
DB 1208 CAGCAGACCAACCCAGCGG 1227
```

RESULT 11  
US-09-364-425B-26  
; Sequence 26, Application US/09364425B  
; Patent No. 6653086  
; GENERAL INFORMATION:  
; APPLICANT: Behan, Dominic P.  
; APPLICANT: Chalmers, Derek T.  
; APPLICANT: Liaw, Chen W.  
; APPLICANT: Lin, I-Lin  
; APPLICANT: Lowitz, Kevin P.  
; APPLICANT: Chen, Ruoping

; TITLE OF INVENTION: Endogenous, Constitutively Activated G Protein-Coupled Orphan Receptor  
; FILE REFERENCE: Aren0047  
; CURRENT APPLICATION NUMBER: US/09/364,425B  
; CURRENT FILING DATE: 2001-12-18  
; PRIOR APPLICATION NUMBER: 60/094,879  
; PRIOR FILING DATE: 1998-07-31  
; PRIOR APPLICATION NUMBER: 60/106,300  
; PRIOR FILING DATE: 1998-10-30  
; PRIOR APPLICATION NUMBER: 60/110,906  
; PRIOR FILING DATE: 1998-12-04  
; PRIOR APPLICATION NUMBER: 60/121,851  
; PRIOR FILING DATE: 1999-02-26  
; NUMBER OF SEQ ID NOS: 60  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 26  
; LENGTH: 1697  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-364-425B-26

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Query Match      11.8%; Score 110; DB 3; Length 1697;
Best Local Similarity 50.2%; Pred. No. 2.6e-14;
Matches 402; Conservative 0; Mismatches 365; Indels 33; Gaps 4;

QY 87 CCTGCTGCTGCTAGGCTGCTGCTCAACAGAGCTGGCGCTCTGGGTGTTCTGCTGCCGAT 146
DB 413 CGTCTGGTGGGCTTCCGGCCAACTGCTGCTCTCTACTTCCGCTACCTGCGAT 472
QY 147 GCAGAGTGGACGAGAGCCCGCATCTCATGACCACTTGGCGGTGGCGGACCTTGGCT 206
DB 473 CAAGCCCGGAAACAGAGCTGGCGGTGCTGCTGCAACCTGACGGTGGCGGACCTTCTTA 532
QY 207 GCTGTGACCTTCCCTTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 266
DB 533 CATCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 592
QY 267 CCAGCTCTCCAGGCGCATCTACCTGACC-----AACAGGTACATGAGCATCAG 314
DB 593 CGACTGTCTGCCAGGTGTGGGATCTCTCTGTACGAGAATCTATACATCAGCGTGG 652
QY 315 CTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 712
DB 375 CGGCTGGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 425
QY 713 CCAGTTCGCGACCTTGAAGGCGCGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 772
DB 426 GCTGTGATCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 485
QY 773 GCTGACAGCATCTACTTCTGATGCAAGAGAGTCTATCGAGGACGAGAACAGCACCG 832
DB 486 CTTGAGGAGCACCGCGCAAAATTTCAACTCCATGCGGTTCGCGTGTGGGATTTACT 545
DB 833 CGTGTGCTTTGAGCATCTACCCCATCCAGCATGGCAGCGCGCATCAACTACTACCGCT 892
QY 546 GCCCTGCGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 605
DB 893 CTTGCTGGGCTTCTCTTCTTCCCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 952
QY 606 ACCC-----ACCGAGCTGGGCGAGGAGGCGCCAGGCTAAACGCGATGCT 656
DB 953 CGCGCTGCGCGGAGCCAGCGCACCCAGAGAGCCGAGAGCATCTGAGCGGCTGCT 1012
QY 657 CTGGGCAACCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 716
DB 1013 GCTGAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1072
QY 717 GCGCTCGAGTGGGCTGGAACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 776
DB 1073 GCGCAGC---GTCTGGGAGGCGAGCTGCGACTTCCGCAAGGCGCTTTTCAACGCGCTACCA 1129
QY 777 CATACACGAGCTCTCAGATGCCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 836
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Db 1130 CTTCTCCCTCTGCTCACCAGCTTCAACTGCTGCGCAGCCCGTCTCTACTGTTCTG 1189

Qy 837 GGCCAAGGAGTTCCAGGAGG 856

Db 1190 CAGCGAGACCAACCCACCGGG 1209

## RESULT 12

```

US-09-170-496D-165
; Sequence 165, Application US/09170496D
; Patent No. 655339
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Liaw, Chen W.
; TITLE OF INVENTION: No. 6553339-Endogenous, Constitutively Activated Human G Protein-
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: AREN-0040
; CURRENT APPLICATION NUMBER: US/09/170,496D
; CURRENT FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 294
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 165
; LENGTH: 1089
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-170-496D-165

```

|                       |              |                  |                 |              |
|-----------------------|--------------|------------------|-----------------|--------------|
| Query Match           | 11.8%        | Score 109.6;     | DB 3;           | Length 1089; |
| Best Local Similarity | 52.5%        | Pred. No. 3e-14; |                 |              |
| Matches 272;          | Conservative | 0;               | Mismatches 234; | Indels 12;   |
| Gaps 1;               |              |                  |                 |              |

|     |    |   |     |
|-----|----|---|-----|
| 98  | Qy | TAGCCTGCTGCTCAACAGCGCTGCGCTCTGGGGTTCCTGCTGCCGATGCGAGTGGA      | 157 |
| 89  | Db | TGGGGCTGCCACCAAATGCTGCTGTGGCGGCTACCGCAGGTGCAACAGCGCA          | 148 |
| 158 | Qy | CGGAGACCCGCACTTACATGACCAACTGGGGGTGGCGGACCTCTGCTGCTGTGCACCT    | 217 |
| 149 | Db | ACGAGCTGGGGCGTCTACTCTGATGAACCTCAGCATCGCGGACCTGTCATCTGCACGC    | 208 |
| 218 | Qy | TGCCCTTCGTGTGTCACCTCCCTCGGAGAC-----ACCTCAGACACGCGCTGT         | 265 |
| 209 | Db | TGCGCTGTGGTGGACTACTTCTGACACAGCAAACTGATCCAGGCCCGGGTCTCT        | 268 |
| 266 | Qy | GCCAGCTCTCCCGAGGGCATCTACTGACCAACAGGTACATGAGCATCAGCCTGTCA      | 325 |
| 269 | Db | GCAAGCTCTTTGGGTTCACTTCTTACACCAATATCTACATCAGCATCGCCTTCTCTGTGCT | 328 |
| 326 | Qy | CCATGCGCGGTGACCGCTATGTGGCCGTGCGGCAACCCGCTGCGTGC               | 385 |
| 329 | Db | GCATCTCGTGGACCGCTACTGTGCTGTGGCCCAACCCCACTCGCTTCGCGCGCTCGGCC   | 388 |
| 386 | Qy | CCCCCAGCAGGCTGCGGCGGTGTGCGGGTCTCTCTGGGTGCTGGTCAATCGGCTCCCTGG  | 445 |
| 389 | Db | GCGTCAAGACCGCGTGGCGCGCTGAGCTCCGTGTGTGTGGGCCACGAGCTGGGGCCAACT  | 448 |
| 446 | Qy | TGGTCTCGCTGGCTCTCGGGGATTCAGGAGGGCGGCTTCTGCTTCAGGAGCAACCGGCACA | 505 |
| 449 | Db | CGGGCCCCCTGTTCATGACGAGCTTTCGAGAGCCGCTTAAACCAACACTTCTGTCTTG    | 508 |
| 506 | Qy | ATTTCAACTCCATGCGGTTC  | 565 |
| 509 | Db | AGAAGTTC  | 568 |
| 566 | Qy | TCGTCTCCCTGAAGTGGTGA  | 603 |
| 569 | Db | TCCTCTTCCGCTGGGCGCTCATGCTGTGCTGTGATACCG                       | 606 |

RESULT 13  
US-09-170-496D-193  
/ Sequence 193, Application US/09170496D

Patent No. 6555339  
GENERAL INFORMATION:  
APPLICANT: Behan, Dominic P.  
APPLICANT: Chalmers, Derek T.  
APPLICANT: Liaw, Chen W.  
TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human C  
TITLE OF INVENTION: Receptors  
FILE REFERENCE: AREN-0040  
CURRENT APPLICATION NUMBER: US/09/170,496D  
CURRENT FILING DATE: 1998-10-13  
NUMBER OF SEQ ID NOS: 294  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 193  
LENGTH: 1128  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-170-496D-193

| Query Match           | 10.0% | Score 92.6   | DB 3           | Length 1128 |
|-----------------------|-------|--|----------------|-------------|
| Best Local Similarity | 47.9% | Pred. No. 1.2e-10  |                |             |
| Matches               | 371   | Conservative 0   | Mismatches 389 | Indels 15   |
| Gaps                  | 3     |  |                |             |
| Qy                    | 66    | CTTCTACGCTACTTGGGCGCTCGTGTGCTAGGCTGCTGTCTACACGCTTGGCGCT        | 125            |             |
| Db                    | 183   | CTGCTGCTCTACACCAATCTTCTCTTCCCATCGGCTTTGTGGCAACATCCTGTATCCT     | 242            |             |
| Qy                    | 126   | CTGGGTGTTCTGTCTCGCGCATGACGAGTGGACCGGACACCGCATCTACATGACCAACCT   | 185            |             |
| Db                    | 243   | GTTGGTGAAATCAGCTTCCGGGAGAAGATGACCATCCCGACCTGTACTTTCATCAACCT    | 302            |             |
| Qy                    | 186   | GGCGTGGCGCACTCTGCTCTGTGTGCACTTTGGCCCTTGTGTGTGCACTCCCT-----     | 239            |             |
| Db                    | 303   | GGCGTGGCGGACCTCATCTCTGTGGCGCATCTCCCTCATTTAGGTGTTCAACCTGCACGA   | 362            |             |
| Qy                    | 240   | GCAGACACCTCAGACACGCGCTGTGCCAGCTCTCCACGGGCATCTACCTGACCAACAG     | 299            |             |
| Db                    | 363   | GGGTACTACGACATCGCGCTCTGTGTGCACTTATGTGCTCTTCTGTGAGGTCAACAT      | 422            |             |
| Qy                    | 300   | GTACATGAGCATCAGCTGTGTCAAGGCCATCGCGTGGACCGCTATGTGGCGTGCAGCA     | 359            |             |
| Db                    | 423   | GTACAGCAGCGTCTTCTTCTCACTCGATGAGCTTCGACCGCTACATCGCCCTGGCCAG     | 482            |             |
| Qy                    | 360   | CCGCTCGTGGCGCGGGCTGCGGTCCCCAGGACGGCTGCGCCGTGTGCGCGGTCTCT       | 419            |             |
| Db                    | 483   | GGCCATGCGTGCAGCTGTTCGCGCAACAGCACACGCCCGGCTGAGCTGTGGCCCTCAT     | 542            |             |
| Qy                    | 420   | CTGGGTCTGGTCACTCGGCTCCCTGGTGGCTCGCTGCTCTCTGGGATTCAGAGAGGGCG    | 479            |             |
| Db                    | 543   | CTGGATGGCATCGTGTGAGCGACGCTGTGTGCCCTTCA CGCCGTGCACCTGTGACGACAC  | 602            |             |
| Qy                    | 480   | CTTCTGTCTCAGGAGCACCGGACAAATTTCAATCCATCGGTTCGCGC-----TGCT       | 533            |             |
| Db                    | 603   | CGACGAGGCTGCTCTGTGTTGGCGATGTCCGGGAGGTGCAGTGGCTCGAGGTCAAGCT     | 662            |             |
| Qy                    | 534   | GGGATTTCACTGCCCTTGGCCGCTGGTGTGCTTCTGTCTCCCTGAAGTGGTGAATGCCCT   | 593            |             |
| Db                    | 663   | GGGCTTCACTGTGCGCTTTCGCCATCATCGGCGTGTGTCTACTCCCTCATGTTCGCGGTGCT | 722            |             |
| Qy                    | 594   | GGGCCAGAGGCCACCCACCGACGCTGGGGGACGAGAGGCCACCGCAAGGTCTAAACGCAT   | 653            |             |
| Db                    | 723   | GGTC--AGGGCGACCGGCACCGTGGCTTGGGCCCCGGGGGAGAGGCAACGCAT          | 779            |             |
| Qy                    | 654   | GGTCTGGGCGCAACTCTGTGTGTGTGTGTGTCTTCTGTCTCCCTGAAGTGGGTGTGAC     | 713            |             |
| Db                    | 780   | GATCTCTCGCGTGTGTGTGTCTTCTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT   | 839            |             |
| Qy                    | 714   | AGTGGCTCTGCAGTGGGCTGGAAACGCTCTGTGCCCTCTCTGAGACGATCGTTCGCGCCT   | 773            |             |
| Db                    | 840   | CGTGACCTCTCGACGGGAGAGAGCTGTGGGCGCTCTCTCTGACGAGCATCTTTCGCGCA    | 899            |             |
| Qy                    | 774   | GTACATAACAGCAAGCTCTCAGATGCCAACTGTGCTCGGACGCCATCTGTCTAC         | 828            |             |
| Db                    | 900   | TGCCACACCCCTCTCAGCGGCCACATTTGCAACCTCGCGCTTCTTCTCAACAGCTGC      | 954            |             |



```

RESULT 14
US-09-170-496D-201
; Sequence 201, Application US/09170496D
; Patent No. 6555339
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Liaw, Chen W.
; TITLE OF INVENTION: No. 6555339--Endogenous, Constitutively Activated Human G Protein-
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: AREN-0040
; CURRENT APPLICATION NUMBER: US/09/170,496D
; CURRENT FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 294
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 201
; LENGTH: 1128
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-170-496D-201

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| Query Match           | 9.8%; Score 91; DB 3; Length 1128;                                     |
|-----------------------|--|
| Best Local Similarity | 47.7%; Pred. No. 2.7e-10;  |
| Matches               | 370; Conservative 0; Mismatches 390; Indels 15; Gaps 3;                |
| QY                    | 66 CTTCTACGCTTACTTGGCGCTGCTGCTAGGCTGCTGCTCAACAGCCTGGCGCT 125           |
| DB                    |  |
| QY                    | 183 CTGCTGCTCTACACCACTTCTTCTCTTCCCCCATCGGCTTTGTGGCAACATCCTGATCCT 242   |
| DB                    |  |
| QY                    | 126 CTGGGTGTTCTGCTGCCGATGACAGTGGACGGAGACCCGCACTACTACATGACCAACCT 185    |
| DB                    |  |
| QY                    | 243 GGTGTGAAATCATAGCTTCCGGGAGAAATGACCATCCCCGACCTGTACTTTCATCAACCT 302   |
| DB                    |  |
| QY                    | 186 GCGGTGGCCGACCTCTGCTGCTGTGCACTTGCCCTTCGTGTGCACTCCCT----- 239        |
| DB                    |  |
| QY                    | 303 GCGGTGGCGGACCTCATCTCTGGTGGCCGACTCCCTCATTTAGAGGTGTTCAACTGTGACGA 362 |
| DB                    |  |
| QY                    | 240 GCGAGACACTCAGACACGCGCTGTGCGAGTCTCCGAGGGCATCTACTGACCAACAG 299       |
| DB                    |  |
| QY                    | 363 GCGGTACTACGACATCGCGCTCTGTGCACTTTCATGTGCTCTTCTCTGAGAGTCAACAT 422    |
| DB                    |  |
| QY                    | 300 GTACATGAGCATCAGCTGCTCAGCGCCATCGCCGTGGACCGCTATGTGGCGCTGCGGCA 359    |
| DB                    |  |
| QY                    | 423 GTACAGCAGCGTCTTCTTCTCACCTGATGAGCTTCGACCGCTACATCGCCCTGGCCAG 482     |
| DB                    |  |
| QY                    | 360 CCGCTGTGTGCGCCGCGGCTGCGGTCCGCCAGGAGGCTGCGGCGGTGTGCGCGGTCTCT 419    |
| DB                    |  |
| QY                    | 483 GGCATATGCTGACGCTTTCGGCACCAAGCACACGCGCGGCTGAGCTGTGGCTCAT 542        |
| DB                    |  |
| QY                    | 420 CTGGGTGTGTGTCATCGGCTCCCTGTGTGCTCGCTGGCTCTCTGGGGAATCAGAGGGCGG 479   |
| DB                    |  |
| QY                    | 543 CTGGATGATCATCGTGTGAGCACACGCTGGTGCCCTTCCCGCGGTGCACTTCGACGACAC 602   |
| DB                    |  |
| QY                    | 480 CTTCTGCTTCAGAGACCCCGGCACAATTTCAACTCCATGCGGTTCCCGC-----TGCT 533     |
| DB                    |  |
| QY                    | 603 CGACGAGGCTGCTTCTGTTTCGCGATGTCGGGAGGTGCAATGGCTCGAGGTCAACGCT 662     |
| DB                    |  |
| QY                    | 534 GGGATTTACTGCGCCCTGGCGGTGTCTTCTGCTCCCTGAGAGGTGTGACTGCGCT 593        |
| DB                    |  |
| QY                    | 663 GGGCTTTCATGCTGTGCCCTTCGCCATCATCGGCTGTGTACTCCTCTCATTTGTCGGGTGCT 722 |
| DB                    |  |
| QY                    | 594 GSCCCAGAGGCCACCCACCGAGTGGGGCAGGACAGAGGCCACCCGCAAGGCTAAACGCAT 653   |
| DB                    |  |
| QY                    | 723 GGTC---AGGGCGCACCGGCACTGTTGGGCTGCGGCCCGCGGCAAGAGCGGAGGCGCAT 779    |
| DB                    |  |
| QY                    | 654 GGTCTGGGCAACCTCTGCTGTTCGTGTCTGTCTTCTCTGCTCCCTGCACTGGGGGTGAC 713    |
| DB                    |  |
| QY                    | 780 GATCTCGGGTGGTGTCTTCTTCTGCTGTCTGCTGGCTGCCGGAACAGTCTTTCATCAG 839     |
| DB                    |  |
| QY                    | 714 AGTGCCTTCGCAATGGGTGGAAAGCCCTGTGCGCTTCTGTGAGACGATCCGTGCGGCCCT 773   |
| DB                    |  |

Db 840 CGTGCACCTCTCTGCAGGGACGACGCTGGGGCGGCTCCCTGCAAGCAGTCTTTCCGCCCA 899  
 Qy 774 GTACATAACACGACGAAGCTCTCAGATGCCAACCTGCTGCTGGAGCCCATTTGCTAC 828  
 Db 900 TGCCCAACCCCTCAGGGGCCACATTGTCACCTCACGGCCTTCTCCAAACAGCTGC 954

RESULT 15  
 US-09-041-545-1  
 ; Sequence 1, Application US/09041545  
 ; Patent No. 6071719  
 ; GENERAL INFORMATION:  
 ; APPLICANT: SATHE, GANESH M.  
 ; APPLICANT: HALSEY, WENDY S.  
 ; APPLICANT: MAO, JOYCE YUE  
 ; TITLE OF INVENTION: ECR 673 : A 7-TRANSMEMBRANE  
 ; TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTOR  
 ; NUMBER OF SEQUENCES: 2  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: RATNER & PRESTIA  
 ; STREET: P.O. BOX 980  
 ; CITY: VALLEY FORGE  
 ; STATE: PA  
 ; COUNTRY: USA  
 ; ZIP: 19482  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: DOS  
 ; SOFTWARE: FastSeq for Windows Version 2.0  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/041,545  
 ; FILING DATE: 11-MAR-1998  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER:  
 ; FILING DATE:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: PRESTIA, PAUL F  
 ; REGISTRATION NUMBER: 23,031  
 ; REFERENCE/DOCKET NUMBER: GP-70414  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 610-407-0700  
 ; TELEFAX: 610-407-0701  
 ; TELEX: 846169  
 ; INFORMATION FOR SEQ ID NO: 1:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 1815 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: cDNA  
 ; US-09-041-545-1

| Query Match           | 9.8%;        | Score 91;   | DB 3;           | Length 1815;       |
|-----------------------|--------------|---|-----------------|--------------------|
| Best Local Similarity | 50.4%;       | Prod. No. 2.9e-10;  |                 |                    |
| Matches 305;          | Conservative | 0;  | Mismatches 290; | Indels 10; Gaps 3; |
| Qy                    | 48           | CCACGGATCAAGCTGGCGCTCTTACGCCCTACTTGGGGCGTCTCGTGTGGTGTCTAGGCGCTGCT | 107             |                    |
| Db                    | 767          | CCAGGCTGTGGCTGGCGCTGATGGCGGTGCACGGAGCCATCTTCTGGCAGGCGTGGT         | 826             |                    |
| Qy                    | 108          | GCTCAACAGCTGGCGCTCTCGGGTGTTCGTGCGCGCATGCAGCAGTGGCAGCGAGACCCG      | 167             |                    |
| Db                    | 827          | GCTCAACGGGCTGGCGCTGTAGCTTCTGTGCGGCACCCGGGGCAAGACACCTCAGT          | 886             |                    |
| Qy                    | 168          | CATCTACATGACCAACTGGGGTGGCGGACCTTGCCTGTGTGTCACCTTGTGCCCTTCGT       | 227             |                    |
| Db                    | 887          | CATCTACACCATCAACTGGTGGTGTGACCGCATCTACTGGTAGGGCTGTCCCTGCCACGCG     | 946             |                    |
| Qy                    | 228          | GTTGCATCCCTTGGCAGACACTCAGACACGCGCGTGTGCCAGCTTCTCCAGGGCATC         | 285             |                    |
| Db                    | 947          | CTTTCGTGTGTACTACGGCGCCAGGGGTGCTCGCGCTGTGCTTTCGCGACGCTCTCGG        | 1006            |                    |



GenCore version 5.1.7  
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OM nucleic - nucleic search, using sw model

Run on: February 11, 2006, 06:08:01 ; Search time 947 Seconds  
(without alignments)

8120.931 Million cell updates/sec

Title: US-10-083-168-84

Perfect score: 930

Sequence: 1 atgaatggcaccctacaacac.....tgtgctgaccctgcctaa 930

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA Main:

- 1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq.\*
- 2: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq.\*
- 3: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq.\*
- 4: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq.\*
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- 7: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq.\*
- 8: /cgn2\_6/ptodata/1/pubpna/US10D\_PUBCOMB.seq.\*
- 9: /cgn2\_6/ptodata/1/pubpna/US10E\_PUBCOMB.seq.\*
- 10: /cgn2\_6/ptodata/1/pubpna/US11\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description         |
|------------|-------|-------------|--------|-------|---------------------|
| 1          | 930   | 100.0       | 930    | 5     | US-10-083-168-84    |
| 2          | 925.2 | 99.5        | 930    | 5     | US-10-083-168-15    |
| 3          | 925.2 | 99.5        | 930    | 5     | US-10-225-567A-491  |
| 4          | 925.2 | 99.5        | 930    | 5     | US-10-696-639-6     |
| 5          | 920.4 | 99.0        | 1875   | 3     | US-09-768-877-21    |
| 6          | 920.4 | 99.0        | 1875   | 5     | US-10-157-031-350   |
| 7          | 920.4 | 99.0        | 49136  | 3     | US-09-768-877-1     |
| 8          | 919   | 98.8        | 1644   | 9     | US-10-505-486-186   |
| 9          | 916.8 | 98.6        | 24477  | 8     | US-10-741-600-17827 |
| 10         | 900   | 96.8        | 1989   | 6     | US-10-101-510-636   |
| 11         | 439.2 | 47.2        | 600    | 10    | US-11-060-756-1687  |
| 12         | 439.2 | 47.2        | 600    | 10    | US-11-060-756-5959  |
| 13         | 200.6 | 21.6        | 201    | 8     | US-10-741-600-61537 |
| 14         | 200.6 | 21.6        | 201    | 8     | US-10-741-600-61547 |
| 15         | 200.6 | 21.6        | 201    | 8     | US-10-741-600-61549 |
| 16         | 200.6 | 21.6        | 201    | 8     | US-10-741-600-61551 |
| 17         | 200.6 | 21.6        | 201    | 8     | US-10-741-600-61552 |
| 18         | 200.6 | 21.6        | 201    | 8     | US-10-741-600-61567 |
| 19         | 200.6 | 21.6        | 201    | 8     | US-10-741-600-61568 |
| 20         | 197.4 | 21.2        | 201    | 8     | US-10-741-600-61525 |
| 21         | 197.4 | 21.2        | 201    | 8     | US-10-741-600-61532 |
| 22         | 197.4 | 21.2        | 201    | 8     | US-10-741-600-61535 |
| 23         | 195.8 | 21.1        | 201    | 8     | US-10-741-600-61565 |

|    |       |      |      |   |                     |                    |
|----|-------|------|------|---|---------------------|--------------------|
| 24 | 172.6 | 18.6 | 201  | 8 | US-10-741-600-61546 | Sequence 61546, A  |
| 25 | 150.6 | 16.2 | 201  | 8 | US-10-741-600-61524 | Sequence 61524, A  |
| 26 | 141.8 | 15.2 | 1854 | 5 | US-09-866-050A-596  | Sequence 596, App  |
| 27 | 141.8 | 15.2 | 1854 | 5 | US-10-152-661-596   | Sequence 596, App  |
| 28 | 111.6 | 12.0 | 1098 | 5 | US-10-251-385-225   | Sequence 225, App  |
| 29 | 111.2 | 12.0 | 1089 | 5 | US-10-251-385-3     | Sequence 3, Appli  |
| 30 | 111.2 | 12.0 | 1089 | 5 | US-10-267-811-1     | Sequence 1, Appli  |
| 31 | 111.2 | 12.0 | 1365 | 6 | US-10-101-510-17    | Sequence 17, Appli |
| 32 | 111.2 | 12.0 | 1365 | 6 | US-10-305-720-1429  | Sequence 1429, Ap  |
| 33 | 111.2 | 12.0 | 1365 | 7 | US-10-283-975A-113  | Sequence 113, App  |
| 34 | 111.2 | 12.0 | 2693 | 3 | US-09-850-948-1     | Sequence 1, Appli  |
| 35 | 111.2 | 12.0 | 2693 | 3 | US-10-273-575-1     | Sequence 1, Appli  |
| 36 | 111.2 | 12.0 | 2696 | 5 | US-10-225-567A-272  | Sequence 272, App  |
| 37 | 111.2 | 12.0 | 2696 | 7 | US-10-712-124-113   | Sequence 113, App  |
| 38 | 111.2 | 12.0 | 2980 | 6 | US-10-101-510-456   | Sequence 456, App  |
| 39 | 110.4 | 11.9 | 1149 | 9 | US-10-450-763-23834 | Sequence 23834, A  |
| 40 | 110.4 | 11.9 | 1617 | 5 | US-10-167-192-2     | Sequence 2, Appli  |
| 41 | 110.4 | 11.9 | 1617 | 6 | US-10-400-991-5     | Sequence 5, Appli  |
| 42 | 110.4 | 11.9 | 1674 | 9 | US-10-505-486-147   | Sequence 147, App  |
| 43 | 110   | 11.8 | 1098 | 3 | US-09-850-948-5     | Sequence 5, Appli  |
| 44 | 110   | 11.8 | 1098 | 5 | US-10-251-385-117   | Sequence 117, App  |
| 45 | 110   | 11.8 | 1098 | 5 | US-10-273-575-5     | Sequence 5, Appli  |

ALIGNMENTS

RESULT 1  
US-10-083-168-84  
; Sequence 84, Application US/10083168  
; Publication No. US20030023069A1  
; GENERAL INFORMATION:  
; APPLICANT: Liaw, Chen W.  
; APPLICANT: Chalmers, Derek T.  
; APPLICANT: Behan, Dominic P.  
; APPLICANT: Maciejewski-Lenior, Dominique  
; APPLICANT: Leonard, James N.  
; APPLICANT: Ortuno, Daniel  
; APPLICANT: Lin, I-Lin  
; TITLE OF INVENTION: Endogenous And No. US20030023069A1-Endogenous, Constitutively Act  
; TITLE OF INVENTION: Receptors  
; FILE REFERENCE: AREN-0320  
; CURRENT APPLICATION NUMBER: US/10/083.168  
; CURRENT FILING DATE: 2002-02-26  
; NUMBER OF SEQ ID NOS: 102  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 84  
; LENGTH: 930  
; TYPE: DNA  
; ORGANISM: Unknown  
; FEATURE:  
; OTHER INFORMATION: No. US20030023069A1el Sequence  
US-10-083-168-84

|                       |                 |   |               |             |
|-----------------------|-----------------|---|---------------|-------------|
| Query Match           | 100.0%          | Score 930;  | DB 5;         | Length 930; |
| Best Local Similarity | 100.0%          | Pred. No. 2.6e-225;   | Mismatches 0; | Indels 0;   |
| Matches 930;          | Conservative 0; | 0;  | Gaps 0;       |             |
| QY                    | 1               | ATGAATGGCACCCTACCAACACCTGTGGCTCCAGCGACCTCAGCTGGCCCCCAGGATCAAG | 60            |             |
| Db                    | 1               | ATGAATGGCACCCTACCAACACCTGTGGCTCCAGCGACCTCAGCTGGCCCCCAGGATCAAG | 60            |             |
| QY                    | 61              | CTGGGCTTCTAGCGCTTCTGGGCTCTGGGCTCTAGGCTCTGCTGCTCAACGCTG        | 120           |             |
| Db                    | 61              | CTGGGCTTCTAGCGCTTCTGGGCTCTGGGCTCTAGGCTCTGCTGCTCAACGCTG        | 120           |             |
| QY                    | 121             | GGCTCTGGGCTTCTGCTGCTGCGCATGCGAGTGGAGCGAGACCGGCACTTACATGACC    | 180           |             |
| Db                    | 121             | GGCTCTGGGCTTCTGCTGCTGCGCATGCGAGTGGAGCGAGACCGGCACTTACATGACC    | 180           |             |
| QY                    | 181             | AACCTGGCGGTGGCGACCTTGTGCTGTGCACTTGGCCCTTGTGTGCTGCACTCCCTG     | 240           |             |
| Db                    | 181             | AACCTGGCGGTGGCGACCTTGTGCTGTGCACTTGGCCCTTGTGTGCTGCACTCCCTG     | 240           |             |

```
QY 241 CGAGACACCTCAGACACGCGCGTGTGCGAGCTCTCCAGGGCATCTACCTGACCAACAGG 300
Db |||||
QY 241 CGAGACACCTCAGACACGCGCGTGTGCGAGCTCTCCAGGGCATCTACCTGACCAACAGG 300
Db |||||
QY 301 TACATGAGCATCAGCCTGTGTCAAGCCATCGCGTGTGACCGCTATGTGGCCGTGCGGCAC 360
Db |||||
QY 301 TACATGAGCATCAGCCTGTGTCAAGCCATCGCGTGTGACCGCTATGTGGCCGTGCGGCAC 360
Db |||||
QY 361 CGCGTGTGTCGCGCGCGTGTGCGCGTGTGCGCGTGTGCGCGTGTGCGCGTGTGCGCGTGTG 420
Db |||||
QY 361 CGCGTGTGTCGCGCGCGTGTGCGCGTGTGCGCGTGTGCGCGTGTGCGCGTGTGCGCGTGTG 420
Db |||||
QY 421 TGGGTGTGTGTATCGGCTCCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 480
Db |||||
QY 421 TGGGTGTGTGTATCGGCTCCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 480
Db |||||
QY 481 TTCTGTCTTCAAGGACACCCCGGCAAAATTTCAAATCTCATGCGGTTCGCGCTGTGGATTC 540
Db |||||
QY 481 TTCTGTCTTCAAGGACACCCCGGCAAAATTTCAAATCTCATGCGGTTCGCGCTGTGGATTC 540
Db |||||
QY 541 TACCTGCCCCGTGCGCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 600
Db |||||
QY 541 TACCTGCCCCGTGCGCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 600
Db |||||
QY 601 AGGCAACCCACCGACGTCGCGGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 660
Db |||||
QY 601 AGGCAACCCACCGACGTCGCGGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 660
Db |||||
QY 661 GCCAACTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 720
Db |||||
QY 661 GCCAACTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 720
Db |||||
QY 721 CTGCGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 780
Db |||||
QY 721 CTGCGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 780
Db |||||
QY 781 ACCAGCAAGCTCTCAGATGCCAACTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 840
Db |||||
QY 781 ACCAGCAAGCTCTCAGATGCCAACTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 840
Db |||||
QY 841 AAGGAGTTCAGGAGGCGTCTGACCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCG 900
Db |||||
QY 841 AAGGAGTTCAGGAGGCGTCTGACCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCG 900
Db |||||
QY 901 CAGGACTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 930
Db |||||
QY 901 CAGGACTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 930
Db |||||

RESULT 2
US-10-083-168-15
; Sequence 15, Application US/10083168
; Publication No. US20030023069A1
; GENERAL INFORMATION:
; APPLICANT: Liaw, Chen W.
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Behan, Dominic P.
; APPLICANT: Maciejewski-Lenior, Dominique
; APPLICANT: Leonard, James N.
; APPLICANT: Ortuno, Daniel
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: Endogenous And No. US20030023069A1-Endogenous, Constitutively Act
; FILE REFERENCE: AREN-0320
; CURRENT APPLICATION NUMBER: US/10/083,168
; CURRENT FILING DATE: 2002-02-26
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 930
; TYPE: DNA
; ORGANISM: Homo sapiens
```

US-10-083-168-15

```
Query Match 99.5%; Score 925.2; DB 5; Length 930;
Best Local Similarity 99.7%; Pred. No. 4.3e-224;
Matches 927; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATGAATGGGACCTTACAAACCTGTGTGCTCCAGGACCTCACCCTGCGCCCGCCAGGATCAAG 60
Db |||||
QY 1 ATGAATGGGACCTTACAAACCTGTGTGCTCCAGGACCTCACCCTGCGCCCGCCAGGATCAAG 60
Db |||||
QY 61 CTGGGCTTCTACGCCCTTACCTGTGGGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 120
Db |||||
QY 61 CTGGGCTTCTACGCCCTTACCTGTGGGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 120
Db |||||
QY 121 GCGCTCTGGGTGTGTGTGTGCGCATGCGAGCATGTGACGAGACCCGCGCATCTACATGACC 180
Db |||||
QY 121 GCGCTCTGGGTGTGTGTGTGCGCATGCGAGCATGTGACGAGACCCGCGCATCTACATGACC 180
Db |||||
QY 181 AACCTGGCGGTGGCGGACCTCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 240
Db |||||
QY 181 AACCTGGCGGTGGCGGACCTCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 240
Db |||||
QY 241 CGAGACACCTCAGACACGCGCGTGTGCGAGCTCTCCAGGGCATCTACCTGACCAACAGG 300
Db |||||
QY 241 CGAGACACCTCAGACACGCGCGTGTGCGAGCTCTCCAGGGCATCTACCTGACCAACAGG 300
Db |||||
QY 301 TACATGAGCATCAGCCTGTGTCAAGCCATCGCGGTCGCGCTATGTGGCCGTGCGGCAC 360
Db |||||
QY 301 TACATGAGCATCAGCCTGTGTCAAGCCATCGCGGTCGCGCTATGTGGCCGTGCGGCAC 360
Db |||||
QY 361 CGCGTGTGTCGCGCGCGTGTGCGCGTGTGCGCGTGTGCGCGTGTGCGCGTGTGCGCGTGTG 420
Db |||||
QY 361 CGCGTGTGTCGCGCGCGTGTGCGCGTGTGCGCGTGTGCGCGTGTGCGCGTGTGCGCGTGTG 420
Db |||||
QY 421 TGGGTGTGTGTATCGGCTCCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 480
Db |||||
QY 421 TGGGTGTGTGTATCGGCTCCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 480
Db |||||
QY 481 TTCTGTCTTCAAGGACACCCCGGCAAAATTTCAAATCTCATGCGGTTCGCGCTGTGGATTC 540
Db |||||
QY 481 TTCTGTCTTCAAGGACACCCCGGCAAAATTTCAAATCTCATGCGGTTCGCGCTGTGGATTC 540
Db |||||
QY 541 TACCTGCCCCGTGCGCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 600
Db |||||
QY 541 TACCTGCCCCGTGCGCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 600
Db |||||
QY 601 AGGCAACCCACCGACGTCGCGGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 660
Db |||||
QY 601 AGGCAACCCACCGACGTCGCGGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 660
Db |||||
QY 661 GCCAACTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 720
Db |||||
QY 661 GCCAACTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 720
Db |||||
QY 721 CTGCGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 780
Db |||||
QY 721 CTGCGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 780
Db |||||
QY 781 ACCAGCAAGCTCTCAGATGCCAACTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 840
Db |||||
QY 781 ACCAGCAAGCTCTCAGATGCCAACTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 840
Db |||||
QY 841 AAGGAGTTCAGGAGGCGTCTGACCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCG 900
Db |||||
QY 841 AAGGAGTTCAGGAGGCGTCTGACCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCG 900
Db |||||
QY 901 CAGGACTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 930
Db |||||
QY 901 CAGGACTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 930
Db |||||

RESULT 3
US-10-225-567A-491
```

Sequence 491, Application US/10225567A  
Publication No. US20030113798A1  
GENERAL INFORMATION:  
APPLICANT: LifeSpan Biosciences  
APPLICANT: Brown, Joseph P.  
APPLICANT: Burner, Glenna C.  
APPLICANT: Roush, Christine L.  
TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS  
FILE REFERENCE: 1920-4-4  
CURRENT APPLICATION NUMBER: US/10/225,567A  
CURRENT FILING DATE: 2001-12-19  
PRIOR APPLICATION NUMBER: 60/257,144  
PRIOR FILING DATE: 2000-12-19  
NUMBER OF SEQ ID NOS: 2292  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 491  
LENGTH: 930  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-225-567A-491

Query Match 99.5%; Score 925.2; DB 5; Length 930;  
Best Local Similarity 99.7%; Pred. No. 4.3e-224;  
Matches 927; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ATGAATGGCACCTAACAACACTGTGGCTCCAGCGACCTCACCTGGCGCCCGCCAGCGCATCAAG 60  
Db 1 ATGAATGGCACCTAACAACACTGTGGCTCCAGCGACCTCACCTGGCGCCCGCCAGCGCATCAAG 60  
Qy 61 CTGGGCTTCTACGCTTACTTGGGCGTCTCTGTGTGTGTAGGCCCTGTGCTCAACAGCGCTG 120  
Db 61 CTGGGCTTCTACGCTTACTTGGGCGTCTCTGTGTGTGTAGGCCCTGTGCTCAACAGCGCTG 120  
Qy 121 GCGCTCTGGGTGTTCTGTGCCGATGCGACGATGGAGCGAGACCCGCGATCTACATGACC 180  
Db 121 GCGCTCTGGGTGTTCTGTGCCGATGCGACGATGGAGCGAGACCCGCGATCTACATGACC 180  
Qy 181 AACCTGGCGGTGGCGGACCTCTGCTGTGTGTGACCTTGCCTTCGTGTGCTGCACTCCCTG 240  
Db 181 AACCTGGCGGTGGCGGACCTCTGCTGTGTGTGACCTTGCCTTCGTGTGCTGCACTCCCTG 240  
Qy 241 CGAGACACCTCAGACACGCCGCTGTGCCAGCTCTCCCAGGCGCATCTACCTGACCAACAGG 300  
Db 241 CGAGACACCTCAGACACGCCGCTGTGCCAGCTCTCCCAGGCGCATCTACCTGACCAACAGG 300  
Qy 301 TACATGAGCATCAGCGCTGGTCA CGGCCATCGCGCGTGAACCGCTATGTGGCCGCGGGCAC 360  
Db 301 TACATGAGCATCAGCGCTGGTCA CGGCCATCGCGCGTGAACCGCTATGTGGCCGCGGGCAC 360  
Qy 361 CGCTGGGTGCGCGGGGCTGGGTCCCGCAGGAGGCTGGCGCGTGTGCGCGTCTCCTC 420  
Db 361 CGCTGGGTGCGCGGGGCTGGGTCCCGCAGGAGGCTGGCGCGTGTGCGCGTCTCCTC 420  
Qy 421 TGGGTGCTGTGTCATCGGCTCCCTGTGTGCTCGCTGGCTCCTTGGGGATTTCAGGAGGGCGC 480  
Db 421 TGGGTGCTGTGTCATCGGCTCCCTGTGTGCTCGCTGGCTCCTTGGGGATTTCAGGAGGGCGC 480  
Qy 481 TTCTGCTTTCAGAGACACCGCGCA CAATTTCAACTCCATGCGGTTCCTCGCTGCTGGATTTC 540  
Db 481 TTCTGCTTTCAGAGACACCGCGCA CAATTTCAACTCCATGCGGTTCCTCGCTGCTGGATTTC 540  
Qy 541 TACCTGCCCTCGGCGGTGTGTCTTCTGCTCCCTGAAAGTGGTGTGACCTGCGCCCGAG 600  
Db 541 TACCTGCCCTCGGCGGTGTGTCTTCTGCTCCCTGAAAGTGGTGTGACCTGCGCCCGAG 600  
Qy 601 AGGCCACCCACCGACGTGGGGCAGGACGAGGCGCACCCGCAAGGCTAAACGCAATGTCTGG 660  
Db 601 AGGCCACCCACCGACGTGGGGCAGGACGAGGCGCACCCGCAAGGCTGCGCGATGTCTGG 660  
Qy 661 GCCAACCTCTGGTGTGTGTGTCTCTGCTCCCTGCGCCCTGACAGTGGGGCTGACAGTGGCG 720  
Db 661 GCCAACCTCTGGTGTGTGTGTGTCTCTGCTCCCTGCGCCCTGACAGTGGGGCTGACAGTGGCG 720

|    |     |  |     |
|----|-----|--|-----|
| Qy | 721 | CTGCAGTGGGCTGGAAAGCGCTCTGTGCGCTCTCTGGAGACGATCCGTGCGCGCCCTGTACATA | 780 |
|    |     |  |     |
| Db | 721 | CTGCAGTGGGCTGGAAAGCGCTGTGTGCGCTCTCTGGAGACGATCCGTGCGCGCCCTGTACATA | 780 |
|    |     |  |     |
| Qy | 781 | ACGAGCAAGCTCTCAGATGCCAACTGCTGCCCTGGACGCCATCTGCTACTACTACATGGCC    | 840 |
|    |     |  |     |
| Db | 781 | ACGAGCAAGCTCTCAGATGCCAACTGCTGCCCTGGACGCCATCTGCTACTACTACATGGCC    | 840 |
|    |     |  |     |
| Qy | 841 | AAGGAGTTCCAGAGGGGCTCTGCACTGGCCCGTGGCTCCCGTGCTAAGGCCCAAAAAGC      | 900 |
|    |     |  |     |
| Db | 841 | AAGGAGTTCCAGAGGGGCTCTGCACTGGCCCGTGGCTCCCGTGCTAAGGCCCAAAAAGC      | 900 |
|    |     |  |     |
| Qy | 901 | CAGGACTCTCTGTGCGTGACCCCTCGCCTAA                                  | 930 |
|    |     |  |     |
| Db | 901 | CAGGACTCTCTGTGCGTGACCCCTCGCCTAA                                  | 930 |
|    |     |  |     |

RESULT 4  
 US-10-696-639-6  
 ; Sequence 6, Application US/10696639  
 ; Publication No. US20050037439A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Pharmacia Corporation  
 ; APPLICANT: Bournier, Maureen J.  
 ; TITLE OF INVENTION: DIFFERENTIALLY EXPRESSED GENES INVOLVED IN CANCER, THE  
 ; TITLE OF INVENTION: POLYPEPTIDES ENCODED THEREBY, AND METHODS OF USING THE SAME  
 ; FILE REFERENCE: 01040/1  
 ; CURRENT APPLICATION NUMBER: US/10/696,639  
 ; CURRENT FILING DATE: 2003-10-29  
 ; PRIOR APPLICATION NUMBER: 60/422,176  
 ; PRIOR FILING DATE: 2002-10-29  
 ; NUMBER OF SEQ ID NOS: 3114  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 6  
 ; LENGTH: 930  
 ; TYPE: DNA  
 ; ORGANISM: homo sapiens  
 US-10-696-639-6

| Query Match           | 99.5% | Score   | 925.2    | DB 8       | Length | 930    |   |      |   |
|-----------------------|-------|---|----------|------------|--------|--------|---|------|---|
| Best Local Similarity | 99.7% | Pred. No.   | 4.3e-224 |            |        |        |   |      |   |
| Matches               | 927   | Conservative  | 0        | Mismatches | 3      | Indels | 0 | Gaps | 0 |
| QY                    | 1     | ATGAATGGCACCTACACACCTATCTTGGGGGCTCTCTGTGTGTCTAGGCTCTGCTCTCAACAGCCTG | 60       |            |        |        |   |      |   |
| DB                    | 1     | ATGAATGGCACCTACACACCTATCTTGGGGCTCTCTGTGTGTCTAGGCTCTGCTCTCAACAGCCTG  | 60       |            |        |        |   |      |   |
| QY                    | 61    | CTGGGCTTCTACGGCTCTATCTTGGGGGCTCTCTGTGTGTCTAGGCTCTGCTCTCAACAGCCTG    | 120      |            |        |        |   |      |   |
| DB                    | 61    | CTGGGCTTCTACGGCTCTATCTTGGGGGCTCTCTGTGTGTCTAGGCTCTGCTCTCAACAGCCTG    | 120      |            |        |        |   |      |   |
| QY                    | 121   | CGGCTCTGGGTGTTCTGTGTCGGCGATGACAGATGTGGACGGAGACCCGGATCTACATGATGCC    | 180      |            |        |        |   |      |   |
| DB                    | 121   | CGGCTCTGGGTGTTCTGTGTCGGCGATGACAGATGTGGACGGAGACCCGGATCTACATGATGCC    | 180      |            |        |        |   |      |   |
| QY                    | 181   | AACCTGGGGGTGGCGGACCTCTGCCTGTCTGTGTGCACCTTTCGCTTCGTGTGCATCTCCCTG     | 240      |            |        |        |   |      |   |
| DB                    | 181   | AACCTGGGGGTGGCGGACCTCTGCCTGTCTGTGTGCACCTTTCGCTTCGTGTGCATCTCCCTG     | 240      |            |        |        |   |      |   |
| QY                    | 241   | CGAGACACCTCAGACACACCGCTGTGCCAGCTCTCCGAGGGGCAATTA                    | 300      |            |        |        |   |      |   |
| DB                    | 241   | CGAGACACCTCAGACACACCGCTGTGCCAGCTCTCCGAGGGGCAATTA                    | 300      |            |        |        |   |      |   |
| QY                    | 301   | TACATGAGCATCAGCGCTGGTCA   | 360      |            |        |        |   |      |   |
| DB                    | 301   | TACATGAGCATCAGCGCTGGTCA   | 360      |            |        |        |   |      |   |
| QY                    | 361   | CGGCTGCTGTCGCCGGGCTGGCGTCCCGCAGGAGGCTCGCGCGCTGTGCGCGTCTCTC          | 420      |            |        |        |   |      |   |
| DB                    | 361   | CGGCTGCTGTCGCCGGGCTGGCGTCCCGCAGGAGGCTCGCGCGCTGTGCGCGTCTCTC          | 420      |            |        |        |   |      |   |
| QY                    | 421   | TGGGTGCTGCTCATCGGGCTCCCTGGTGGCTCGCTGGCTCTCTGGGGATTCAGAGGGCGGC       | 480      |            |        |        |   |      |   |

Db 421 TGGGTGCTGTCATCGGCTCCCTGGTGGCTCGCTGGCTCCTGGGATTTCAGAGGGCGGC 480  
QY 481 TTCTGCTTCAGAGACACCCGGGCAAAATTCACTCCATGCGGTCCCGCTGCTGGGATTTC 540  
Db 481 TTCTGCTTCAGAGACACCCGGGCAAAATTCACTCCATGCGGTTCGCGCTGCTGGGATTTC 540  
QY 541 TACCTGCCCCCTGGCGGTGGTGGTCTTCTGCTCCCTGAAGGTGGTGAATGCTGGCCCCAG 600  
Db 541 TACCTGCCCCCTGGCGGTGGTGGTCTTCTGCTCCCTGAAGGTGGTGAATGCTGGCCCCAG 600  
QY 601 AGGCCACCCACCGACGCTGGGGGAGGAGAGCCACCCGCAAGGCTAAACGATGCTGG 660  
Db 601 AGGCCACCCACCGACGCTGGGGGAGGAGAGCCACCCGCAAGGCTGGCCCCGATGGTCTGG 660  
QY 661 GCACAACTCTCTGCTGGTGGTGGTCTTCTGCTCCCTGCAAGGTGGTGAATGCTGGCCCC 720  
Db 661 GCACAACTCTCTGCTGGTGGTGGTCTTCTGCTCCCTGCAAGGTGGTGAATGCTGGCCCC 720  
QY 721 CTGCGAGTGGGCTGGGAACGCTGTCGCTCCCTGCGAGACGATCCGTCGCGCCCTGTACATA 780  
Db 721 CTGCGAGTGGGCTGGGAACGCTGTCGCTCCCTGCGAGACGATCCGTCGCGCCCTGTACATA 780  
QY 781 ACCAGCAAGCTCTCAGATGCCAACTGCTGCTGGAGCCCATCTGCTACTACTACATGGCC 840  
Db 781 ACCAGCAAGCTCTCAGATGCCAACTGCTGCTGGAGCCCATCTGCTACTACTACATGGCC 840  
QY 841 AAGAGTTCAGAGGCGTCTGCACTGGCCGCTGCTGCTCCCGTCCCGTGAAGGCCCAAAAGC 900  
Db 841 AAGAGTTCAGAGGCGTCTGCACTGGCCGCTGCTGCTCCCGTCCCGTGAAGGCCCAAAAGC 900  
QY 901 CAGGACTCTCTGTCGCTGAGCCCTCGCCTAA 930  
Db 901 CAGGACTCTCTGTCGCTGAGCCCTCGCCTAA 930

## RESULT 5

US-09-768-877-21

; Sequence 21, Application US/09768877

; Patent No. US20020150896A1

; GENERAL INFORMATION:

; APPLICANT: POLONSKY, KENNETH S.

; APPLICANT: HORIKAWA, YUKIO

; APPLICANT: ODA, NAHISA

; APPLICANT: COX, NANCY J.

; APPLICANT: SREENAN, SEAMUS

; APPLICANT: ZHOU, YUN-PING

; APPLICANT: OTANI, KENICHI

; APPLICANT: HANIS, CRAIG L.

; APPLICANT: BELL, GRAEME I.

; TITLE OF INVENTION: METHODS OF TREATMENT OF TYPE 2 DIABETES

; FILE REFERENCE: ARCD:307

; CURRENT APPLICATION NUMBER: US/09/768,877

; CURRENT FILING DATE: 2001-01-23

; PRIOR APPLICATION NUMBER: 09/422,869

; PRIOR FILING DATE: 1999-10-21

; NUMBER OF SEQ ID NOS: 30

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 21

; LENGTH: 1875

; TYPE: DNA

; ORGANISM: Human

US-09-768-877-21

Query Match 99.0%; Score 920.4; DB 3; Length 1875;

Best Local Similarity 99.4%; Pred. No. 7.1e-223;

Matches 924; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 ATGAATGGCACTTACAAACCTGTGGCTCAGGACCTCACTGGGCCCGCCAGGATCAAG 60

Db 576 ATGAATGGCACTTACAAACCTGTGGCTCAGGACCTCACTGGGCCCGCCAGGATCAAG 635

QY 61 CTGGGCTTCTACGCTACTTGGGCTCTGCTGGTCTAGGCTGCTGCTCAACAGCTG 120

Db 636 CTGGGCTTCTACGCTACTTGGGCGTCTGCTGGTCTAGGCTGCTGCTCAACAGCGTG 695  
QY 121 GGCTCTGGGTGTTCTGCTGCGCATGCAAGAGTGAACGAGACCCGCACTCTACATGACC 180  
Db 696 GGCTCTGGGTGTTCTGCTGCGCATGCAAGAGTGAACGAGACCCGCACTCTACATGACC 755  
QY 181 AACCTGGCGGTGGCGACCTCTGCTGCTGCAACCTTGGCTGCTGCTGCTGCTGCTGCTG 240  
Db 756 AACCTGGCGGTGGCGACCTCTGCTGCTGCAACCTTGGCTGCTGCTGCTGCTGCTGCTG 815  
QY 241 CAGAGACCTCTCAGACACGCGCTGTGCCAGCTCTCCACAGGCACTACCTGACCAACAGG 300  
Db 816 CAGAGACCTCTCAGACACGCGCTGTGCCAGCTCTCCACAGGCACTACCTGACCAACAGG 875  
QY 301 TACATGAGCATACAGCTGCTCAGGCAATGCGCTGGAACGCTATATGCGCTGCGGCGAC 360  
Db 876 TACATGAGCATACAGCTGCTCAGGCAATGCGCTGGAACGCTATATGCGCTGCGGCGAC 935  
QY 361 CGCTCGCTGCGCGGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCT 420  
Db 936 CGCTCGCTGCGCGGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCT 995  
QY 421 TGGGTGCTGCTCATCGGCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480  
Db 996 TGGGTGCTGCTCATCGGCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1055  
QY 481 TTCTGCTTCAGAGACACCCGGGCAAAATTCACTCCATGCGGTTCGCTGCTGCTGCTGCTG 540  
Db 1056 TTCTGCTTCAGAGACACCCGGGCAAAATTCACTCCATGCGGTTCGCTGCTGCTGCTGCTG 1115  
QY 541 TACCTGCGCTGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600  
Db 1116 TACCTGCGCTGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1175  
QY 601 AGGCCACCCACCGAGCTGGGGCAGGAGGCGCACCCGCAAGGCTAAACGCACTGGTCTGG 660  
Db 1176 AGGCCACCCACCGAGCTGGGGCAGGAGGCGCACCCGCAAGGCTGGCGCATGGTCTGG 1235  
QY 661 GCCAACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720  
Db 1236 GCCAACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1295  
QY 721 CTGCGAGTGGGCTGGAAACGCTGCGCTGCGCTGCGAGACGATCCGTCGCGCCCTGTACATA 780  
Db 1296 CTGCGAGTGGGCTGGAAACGCTGCGCTGCGCTGCGAGACGATCCGTCGCGCCCTGTACATA 1355  
QY 781 ACCAGCAAGCTCTCAGATGCCAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840  
Db 1356 ACCAGCAAGCTCTCAGATGCCAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1415  
QY 841 AAGGAGTTCAGAGGCGCTTGCATGCGCGTGGCTTCCCGCTGCTGCTGCTGCTGCTGCTGCTG 900  
Db 1416 AAGGAGTTCAGAGGCGCTTGCATGCGCGTGGCTTCCCGCTGCTGCTGCTGCTGCTGCTGCTG 1475  
QY 901 CAGGACTCTCTGCTGCTGAGCCCTCGCCTAA 930  
Db 1476 CAGGACTCTCTGCTGCTGAGCCCTCGCCTAA 1505

## RESULT 6

US-10-157-031-350

; Sequence 350, Application US/10157031

; Publication No. US20030108990A1

; GENERAL INFORMATION:

; APPLICANT: Baranova, A. V.

; APPLICANT: Yankovsky, N. K.

; APPLICANT: Kozlov, A. P.

; APPLICANT: Lobashnev, A. V.

; APPLICANT: Krukovskaya, L. L.

; TITLE OF INVENTION: In silico screening for phenotype-associated expressed sequences

; FILE REFERENCE: 2760-103

; CURRENT APPLICATION NUMBER: US/10/157,031

; CURRENT FILING DATE: 2002-05-30









QY 779 TAACGAGAGCTCTCAGATGCCAACTGCTGCGCTGGAGCCATCTGTACTACTACATGG 838  
DB 994 TAACGAGAGAGCTCTCAGATGCCAACTGCTGCGCTGGAGCCATCTGTACTACTACATGG 1053  
QY 839 CCAAGAGATTCCAGGAGCGCTCTGCACTGGCCGCTGGCTCCCGCTGCTTAAGGCCACAAAA 898  
DB 1054 CCAAGAGATTCCAGGAGCGCTCTGCACTGGCCGCTGGCTCCCGCTGCTTAAGGCCACAAAA 1113  
QY 899 GCAGAGACTCTCTGTGGTGAACCTCGCCTAA 930  
DB 1114 GCCAGGACTCTCTGTGGTGAACCTCGCCTAA 1145

## RESULT 11

US-11-060-756-1687  
; Sequence 1687, Application US/11060756  
; Publication No. US20050221354A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounts, William Martin  
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug  
; FILE REFERENCE: AM101083 (031896-042000)  
; CURRENT APPLICATION NUMBER: US/11/060,756  
; CURRENT FILING DATE: 2005-02-18  
; NUMBER OF SEQ ID NOS: 303284  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 1687  
; LENGTH: 600  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-11-060-756-1687

Query Match 47.2%; Score 439.2; DB 10; Length 600;  
Best Local Similarity 99.3%; Pred. No. 3.1e-101;  
Matches 441; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 487 TTCAGAGACACCGGACAAATTTCAACTCCATGCGGTTCCTGCTGGGATTTCTACCTG 546  
DB 1 TTCAGAGACACCGGACAAATTTCAACTCCATGCGGTTCCTGCTGGGATTTCTACCTG 60  
QY 547 CCCTGGCGGTGTGCTCTGCTCCCTGAAAGGTGTGACTGCCCTGCCAGAGGCCA 606  
DB 61 CCCTGGCGGTGTGCTCTGCTCCCTGAAAGGTGTGACTGCCCTGCCAGAGGCCA 120  
QY 607 CCACCGAGCTGGGGCAGGAGGCCACCGCAAGGCTAAAGCATGGTCTGGGCCAAC 666  
DB 121 CCACCGAGCTGGGGCAGGAGGCCACCGCAAGGCTAAAGCATGGTCTGGGCCAAC 180  
QY 667 CTCTGGTGTGTGCTGCTCTGCTCCCTGAAAGGTGTGACTGCCCTGCCAGAGGCCA 726  
DB 181 CTCTGGTGTGTGCTGCTCTGCTCCCTGAAAGGTGTGACTGCCCTGCCAGAGGCCA 240  
QY 727 GTGGGCTGGAAAGCGCTGTGCTCCCTCTGGAGAGCATCCGTGGCGCCCTGTACATAACAGC 786  
DB 241 GTGGGCTGGAAAGCGCTGTGCTCCCTCTGGAGAGCATCCGTGGCGCCCTGTACATAACAGC 300  
QY 787 AAGCTCTCAGATGCCAAGCTGCTGCTGCCCTGGAGCGCATCTGTACTACTACATGGCCAGGAG 846  
DB 301 AAGCTCTCAGATGCCAAGCTGCTGCTGCCCTGGAGCGCATCTGTACTACTACATGGCCAGGAG 360  
QY 847 TTCAGAGAGCGTCTGCACTGGCGGTTCCTGCTCCCTGCAAGGTGGTGAAGGCCACAAAAAGCCAGGAC 906  
DB 361 TTCAGAGAGCGTCTGCACTGGCGGTTCCTGCTCCCTGCAAGGTGGTGAAGGCCACAAAAAGCCAGGAC 420  
QY 907 TCTCTGTGGTGAACCTCGCCTAA 930  
DB 421 TCTCTGTGGTGAACCTCGCCTAA 444

## RESULT 12

US-11-060-756-5959

; Sequence 5959, Application US/11060756  
; Publication No. US20050221354A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounts, William Martin  
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug  
; FILE REFERENCE: AM101083 (031896-042000)  
; CURRENT APPLICATION NUMBER: US/11/060,756  
; CURRENT FILING DATE: 2005-02-18  
; NUMBER OF SEQ ID NOS: 303284  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 5959  
; LENGTH: 600  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-11-060-756-5959

Query Match 47.2%; Score 439.2; DB 10; Length 600;  
Best Local Similarity 99.3%; Pred. No. 3.1e-101;  
Matches 441; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 487 TTCAGAGACACCGGACAAATTTCAACTCCATGCGGTTCCTGCTGGGATTTCTACCTG 546  
DB 1 TTCAGAGACACCGGACAAATTTCAACTCCATGCGGTTCCTGCTGGGATTTCTACCTG 60  
QY 547 CCCTGGCGGTGTGCTCTGCTCCCTGAAAGGTGTGACTGCCCTGCCAGAGGCCA 606  
DB 61 CCCTGGCGGTGTGCTCTGCTCCCTGAAAGGTGTGACTGCCCTGCCAGAGGCCA 120  
QY 607 CCACCGAGCTGGGGCAGGAGGCCACCGCAAGGCTAAAGCATGGTCTGGGCCAAC 666  
DB 121 CCACCGAGCTGGGGCAGGAGGCCACCGCAAGGCTAAAGCATGGTCTGGGCCAAC 180  
QY 667 CTCTGGTGTGTGCTGCTCTGCTCCCTGAAAGGTGTGACTGCCCTGCCAGAGGCCA 726  
DB 181 CTCTGGTGTGTGCTGCTCTGCTCCCTGAAAGGTGTGACTGCCCTGCCAGAGGCCA 240  
QY 727 GTGGGCTGGAAAGCGCTGTGCTCCCTCTGGAGAGCATCCGTGGCGCCCTGTACATAACAGC 786  
DB 241 GTGGGCTGGAAAGCGCTGTGCTCCCTCTGGAGAGCATCCGTGGCGCCCTGTACATAACAGC 300  
QY 787 AAGCTCTCAGATGCCAAGCTGCTGCTGCCCTGGAGCGCATCTGTACTACTACATGGCCAGGAG 846  
DB 301 AAGCTCTCAGATGCCAAGCTGCTGCTGCCCTGGAGCGCATCTGTACTACTACATGGCCAGGAG 360  
QY 847 TTCAGAGAGCGTCTGCACTGGCGGTTCCTGCTCCCTGCAAGGTGGTGAAGGCCACAAAAAGCCAGGAC 906  
DB 361 TTCAGAGAGCGTCTGCACTGGCGGTTCCTGCTCCCTGCAAGGTGGTGAAGGCCACAAAAAGCCAGGAC 420  
QY 907 TCTCTGTGGTGAACCTCGCCTAA 930  
DB 421 TCTCTGTGGTGAACCTCGCCTAA 444

## RESULT 13

US-10-741-600-61537  
; Sequence 61537, Application US/10741600  
; Publication No. US20050026169A1  
; GENERAL INFORMATION:  
; APPLICANT: CARGILL, Michele et al.  
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
; FILE REFERENCE: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF  
; CURRENT APPLICATION NUMBER: US/10/741,600  
; CURRENT FILING DATE: 2003-12-22  
; NUMBER OF SEQ ID NOS: 73997  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 61537  
; LENGTH: 201  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-741-600-61537

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Query Match      21.6%; Score 200.6; DB 8; Length 201;
Best Local Similarity 99.5%; Pred. No. 6.4e-41;
Matches 200; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 223 TTCTGTCTGCACTCCCTCGAGACACCTTCAGACACGCGCTGTGCTCCAGCTTCCAGGCG 282
Db 1 TTCTGTCTGCACTCCCTCGAGACACCTTCAGACACGCGCTGTGCTCCAGCTTCCAGGCG 60

Qy 283 ATCTACCTGACCAACAGGTATACATGAGCATGAGCTGTGCTCCAGGCGCATGCGTGACCGC 342
Db 61 ATCTACCTGACCAACAGGTATACATGAGCATGAGCTGTGCTCCAGGCGCATGCGTGACCGC 120

Qy 343 TATGTGCGCGGCGGCGACCGCTGCTGCGCGCGGCTGCGGTCCTCCAGGCGAGCTGCG 402
Db 121 TATGTGCGCGGCGGCGACCGCTGCTGCGCGCGGCTGCGGTCCTCCAGGCGAGCTGCG 180

Qy 403 GCCGTGTGCGCGGTCCTCTGG 423
Db 181 GCCGTGTGCGCGGTCCTCTGG 201

RESULT 14
US-10-741-600-61547
; Sequence 61547, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001499
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 61547
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-741-600-61547

Query Match      21.6%; Score 200.6; DB 8; Length 201;
Best Local Similarity 99.5%; Pred. No. 6.4e-41;
Matches 200; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 23 GTGGCTCCAGCGACCTCACTGGCCCCCAGCGCATCAAGCTGGGCTTCTACGCTTACTTGG 82
Db 1 GTGGCTCCAGCGACCTCACTGGCCCCCAGCGCATCAAGCTGGGCTTCTACGCTTACTTGG 60

Qy 83 GCGTCTGTGTGTGTAGGCTGTGCTCAACAGCGCTGGCGCTCTGGGTGTCTGTCTGCC 142
Db 61 GCGTCTGTGTGTGTAGGCTGTGCTCAACAGCGCTGGCSCTCTGGGTGTCTGTCTGCC 120

Qy 143 GCATCAGCAGTGGACGGAGCCCGCATCTACATCAACAACTGGCGTGGCGGACCTCT 202
Db 121 GCATCAGCAGTGGACGGAGCCCGCATCTACATCAACAACTGGCGTGGCGGACCTCT 180

Qy 203 GCGTCTGTGCACTTGGCCCT 223
Db 181 GCGTCTGTGCACTTGGCCCT 201

RESULT 15
US-10-741-600-61549
; Sequence 61549, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001499
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
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; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 61549
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-741-600-61549

Query Match      21.6%; Score 200.6; DB 8; Length 201;
Best Local Similarity 99.5%; Pred. No. 6.4e-41;
Matches 200; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 276 CCAGGGCATCTTACCTGACCAACAGGTATACATGAGCATCAGCTGTGTCAGGGCATCGCGT 335
Db 1 CCAGGGCATCTTACCTGACCAACAGGTATACATGAGCATCAGCTGTGTCAGGGCATCGCGT 60

Qy 336 GGACCGCTATGTGGCGGTGGGCAACCGCTGCGTGGCGGCTGCGGTCCTCCAGGCA 395
Db 61 GGACCGCTATGTGGCGGTGGGCAACCGCTGCGTGGCGGCTGCGGTCCTCCAGGCA 120

Qy 396 GGCTGCGGCGGTGTGCGGCTCTCTGGGTCTGCTCATCGGCTTCCCTGTGGTGGCTCGCTG 455
Db 121 GGCTGCGGCGGTGTGCGGCTCTCTGGGTCTGCTCATCGGCTTCCCTGTGGTGGCTCGCTG 180

Qy 456 GCTCTGGGGATTTCAGGAGGG 476
Db 181 GCTCTGGGGATTTCAGGAGGG 201
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Search completed: February 11, 2006, 09:51:07  
Job time : 948 secs

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| Result No. | Score | Query |       | Length | DB                  | ID                  | Description       |
|------------|-------|-------|-------|--------|---------------------|---------------------|-------------------|
|            |       | Match |       |        |                     |                     |                   |
| 1          | 110   | 11.8  | 1523  | 11     | US-11-137-877-30    |                     | Sequence 30, Appl |
| 2          | 89    | 9.6   | 1238  | 7      | US-10-995-561-321   |                     | Sequence 321, App |
| 3          | 89    | 9.6   | 1498  | 7      | US-10-995-561-320   |                     | Sequence 320, App |
| 4          | 89    | 9.6   | 2095  | 7      | US-10-750-185-61969 |                     | Sequence 61969, A |
| 5          | 89    | 9.6   | 2095  | 7      | US-10-750-623-61969 |                     | Sequence 61969, A |
| 6          | 89    | 9.6   | 86131 | 7      | US-10-995-561-13298 |                     | Sequence 13298, A |
| C          | 7     | 88.2  | 9.5   | 1685   | 7                   | US-10-750-185-36071 | Sequence 36071, A |
|            | 8     | 88.2  | 9.5   | 1685   | 7                   | US-10-750-623-36071 | Sequence 36071, A |
| 9          | 84.2  | 9.1   | 1077  | 11     | US-11-127-877-29    |                     | Sequence 29, Appl |
| 10         | 75.2  | 8.1   | 2011  | 11     | US-11-136-527-3805  |                     | Sequence 3805, Ap |
| C          | 11    | 74.2  | 8.0   | 706    | 7                   | US-10-750-185-32790 | Sequence 32790, A |
| 12         | 74.2  | 8.0   | 706   | 7      | US-10-750-623-32790 |                     | Sequence 32790, A |
| 13         | 73    | 7.8   | 1278  | 11     | US-11-136-527-3310  |                     | Sequence 3310, Ap |
| 14         | 72.4  | 7.8   | 1428  | 7      | US-10-995-561-28    |                     | Sequence 28, Appl |
| 15         | 72.4  | 7.8   | 13428 | 7      | US-10-995-561-13208 |                     | Sequence 13208, A |
| 16         | 72.2  | 7.8   | 4267  | 11     | US-11-127-877-15    |                     | Sequence 15, Appl |
| 17         | 71.8  | 7.7   | 2955  | 11     | US-11-136-527-2954  |                     | Sequence 2954, Ap |
| 18         | 71.6  | 7.7   | 1290  | 11     | US-11-136-527-2457  |                     | Sequence 2457, Ap |
| 19         | 71.6  | 7.7   | 1290  | 11     | US-11-136-527-6553  |                     | Sequence 6553, Ap |
| 20         | 71    | 7.6   | 3023  | 11     | US-11-127-877-22    |                     | Sequence 22, Appl |
| 21         | 71    | 7.6   | 3418  | 11     | US-11-136-527-3778  |                     | Sequence 3778, Ap |

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Db 610 CGACCTGTCTCTGCGCAGGTGTGGGCATCTCTCTGTACGAGAACATCTACATCAGCGTGGG 669
Qy 315 CTGTGTCACGGCCATCGCGTGTGACCGCTATGTGGCGGTGGGCACCCCGTGGTGGCCGG 374
Db 670 CTTCTCTCTGTGATCTCTGCTGACCGCTACCTGGCTGTGGCCATCTCCCTTCGGCTTCCA 729
Qy 375 CGGGCTGGCGTCCCGCAGGCGAGCTGGGCGGTGTGGGGTCTCTGGG-----T 425
Db 730 CAGTTCCGAGCCCTGAGCGGCCCTGGCGTACAGGTGTGATCTGGGCCAAGAGCT 789
Qy 426 GTGTGTATCGGCTCCCTGTGTGCTCTGGCTGTCTCTGGGATTTCAGAGGGGGGCTTTG 485
Db 790 GCTGACGAGCATCTCTCTGTATGATCAAGAGAGGTCTATCGAGGAGAGAACGAGCACCG 849
Qy 486 CTTTACGAGGACCGCGGACAAATTTCAATCTCATGTGGTTCCCGCTCTCTGGGATTTTACT 545
Db 850 CGTGTGCTTTGAGCACTACCCCATCCAGGATGGCAGCGCGCCATCAACTACTACCGCTT 909
Qy 546 GCGCTGGCGGTGGTCTCTCTGCTCCCTGAAGTGTGATCTGCGCTGGCCCGCAGAGGCC 605
Db 910 CTTGTGGGCTTCTCTCTCCCATCTGCTGTCTGTGGGTCTTACCGAGGATCTCTGG 969
Qy 606 ACCC-----ACCGAGTGGGGCAGGCGAGAGGCCACCGCAAGGCTAAACGCAATGT 656
Db 970 CGCGGTGGCGGAGCCACGGCACCCAGAGAGCGCGAAGGACCATCCAGCGCTGT 1029
Qy 657 CTGGGCGAACCTCTCTGGTGTGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 716
Db 1030 GCTCAGCAGCGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1089
Qy 717 GCGCTCGCAGTGGGTGGAAGCGCTGTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 776
Db 1090 GCGCAGC---GTCTGGAGCGCAGCTGCGACTTTCGCAAGGGGGTTCCTCAAGCGCTTACCA 1146
Qy 777 CATAACGAGCAAGCTCTCAGATGCCAACTGCTGCTGCGAGCGCATCTGCTACTACTACAT 836
Db 1147 CTTCTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1206
Qy 837 GGCACAGGAGTTCCAGAGG 856
Db 1207 CAGCGAGACCAACCGCGG 1226
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## RESULT 2

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US-10-995-561-321
; Sequence 321, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 321
; LENGTH: 1238
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-321
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Query Match 9.6%; Score 89; DB 7; Length 1238;
Best Local Similarity 55.5%; Pred. No. 5e-09;
Matches 217; Conservative 0; Mismatches 165; Indels 9; Gaps 2;

Qy 45 GCGCCGAGGATCAAGCTGGGCTTCTACGCTACTCTTGGGCGTCTCTGCTGTCTAGGCTT 104
Db 197 GCGGCGGCGGCGATGCTGCTATCCAGTATCTACGCTTCTGCGCGTCTGCTGTGGGCT 256
Qy 105 GCTGCTCAACAGCCTGGCGCTCTGGGTGTCTGCTGCGCGCATGACAGAGTGGACGAGAC 164
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Db 257 GGTGGGCGAACGCCCTGGTCTATCTTCTGTATCGCTACGCCAAGATGAAGACGGCTAC 316
Qy 165 CGCATCTACATGACCAACCTGGCGGTGGCGGACCTCTGCTGCTGTGTGACACTTGGCCCTT 224
Db 317 CAMCATCTACCTGCTCAACCTGGCGGTAGCGGACGAGCTCTTCTATGCTGAGCGTGCCTT 376
Qy 225 CGT-----GCTGCACTCCCTGGCGAGAC---ACCTCAGACAGCGCGCTGTGCCAGCTCTC 275
Db 377 CGTGGCCTGCTGCGCGCCCTGGCCACTGGCCCTTCGGCTCCGTGCTGTGCGCGCGGT 436
Qy 276 CCAGGGCATCTACCTGACCAACAGGATACATGAGCATCAGCCTGTGTCAGGGCCATCGCGT 335
Db 437 GCTCAGCGTGCAGCGCCTCAACATGTTACCAGCGTCTTCTGCTCTACCGTCTCAGCGT 496
Qy 336 GGAACGCTATGTGGCGGTGGCGGACCCCGTGGTGGCGCGGCGTGGCGTCCCCCAGGCA 395
Db 497 GGACCGCTACGTGGCGGTGGTGGTGCACCTCTGCGCGCGCGACCTTACCGCGCGCCAGCGT 556
Qy 396 GGCTGGCGCGGTGTGGCGGTCTCTTGGGTG 426
Db 557 GGCCAAAGCTCATCAACCTGGCGGTGTGGTG 587
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## RESULT 3

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US-10-995-561-320
; Sequence 320, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 320
; LENGTH: 1498
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-320
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Query Match 9.6%; Score 89; DB 7; Length 1498;
Best Local Similarity 55.5%; Pred. No. 5.1e-09;
Matches 217; Conservative 0; Mismatches 165; Indels 9; Gaps 2;

Qy 45 GCGCCGAGGATCAAGCTGGGCTTCTACGCTTCTGCGCGTCTGCTGTGCTAGGCTT 104
Db 197 GCGGCGGCGGCGATGCTGCTATCCAGTATCTACGCTTCTGCGCGTCTGCTGTGGGCT 256
Qy 105 GCTGCTCAACAGCCTGGCGCTCTGGGTGTCTGCTGCGCGCATGACAGAGTGGACGAGAC 164
Db 257 GGTGGGCGAACGCCCTGGTCTATCTTCTGATCTTCTGCTACGCCAAGATGAAGACGGCTAC 316
Qy 165 CGCATCTACATGACCAACCTGGCGGTGGCGGACCTCTGCTGCTGTGTGACACTTGGCCCTT 224
Db 317 CAMCATCTACCTGCTCAACCTGGCGGTAGCGGACGAGCTCTTCTATGCTGAGCGTGCCTT 376
Qy 225 CGT-----GCTGCACTCCCTGGCGAGAC---ACCTCAGACAGCGCGCTGTGCCAGCTCTC 275
Db 377 CGTGGCCTGCTGCGCGCCCTGGCCACTGGCCCTTCGGCTCCGTGCTGTGCGCGCGGT 436
Qy 276 CCAGGGCATCTACCTGACCAACAGGATACATGAGCATCAGCCTGTGTCAGGGCCATCGCGT 335
Db 437 GCTCAGCGTGCAGCGCCTCAACATGTTACCAGCGTCTTCTGCTCTACCGTCTCAGCGT 496
Qy 336 GGAACGCTATGTGGCGGTGGCGGACCCCGTGGTGGCGCGGCGTGGCGTCCCCCAGGCA 395
Db 497 GGACCGCTACGTGGCGGTGGTGGTGCACCTCTGCGCGCGCGACCTTACCGCGCGCCAGCGT 556
Qy 396 GGCTGGCGCGGTGTGGCGGTCTCTTGGGTG 426
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Db 557 GGCCAAAGTCAATCAACCTGGCGTGTGGCTG 587

RESULT 4
US-10-750-185-61969
; Sequence 61969, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: NM1100-2
; CURRENT APPLICATION NUMBER: US/10750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 61969
; LENGTH: 2095
; TYPE: DNA
; ORGANISM: Bovine 19866880917942
; US-10-750-185-61969

Query Match 9.6%; Score 89; DB 7; Length 2095;
Best Local Similarity 47.9%; Pred. No. 5.3e-09;
Matches 402; Conservative 0; Mismatches 410; Indels 27; Gaps 4;

Qy 20 CCTGTGGCTCCAGGACCTCACTGGCCCCCAGGATCAAGCTGGGCTTCTACGGCTACT 79
Db 493 CCGTGTCTTCTTGGCACCCGCCCTCTCCCATAGTGTCTGCCCTCTTCTATCTTCTGCT 552
Qy 80 TGGGGCTCTGCTGGTGTAGGCTGTCTCAACAGCTGGCGCTCTGGGTGTTCTGCT 139
Db 553 TGGGCATGGAGTTTGTCTGGGCTGTGGGGAACAGGCTGTCCTTCTTCTTCTGCT 612
Qy 140 GCCGATGACAGTGGAGCGAGACCCGCATCTACATGACCAACCTGGCGGTGGCGACC 199
Db 613 TGGGACCGGCGCTTGGAGCTTCAACACCGTGTCTCTGTCAGCTTGGTGGTGGCGACT 672
Qy 200 TCTGCTCTGTGCACTTGGCTTGTGTCATCTCCCTGGGAGACCTCAGACACGC 259
Db 673 TCTCTCTGATCTCAACCTGGCCCTTCCGCTGGATTACTTCTTCCACGAGATCTGCG 732
Qy 260 -----CGTGTGCCAGCTCTCCAGGAGATCTTCTGATGCCACCAACCGGACCA 307
Db 733 GCTTTGGGGACACCGCCCTGCAAGTCAACCTGTTCATGATGCCACCAACCGGACCA 792
Qy 308 GCATCAGCTGTGACGCGCATCGCGCTGACCGCTATGTGCGCGTGGCGACCCGCTGC 367
Db 793 GCGTGGTCTTCTCAAGCGCGTGGCGCTCAACCGCTACTTGAAGTGGGTGGCGCACACC 852
Qy 368 GTGCCCGGGGTGGCGTCCCCAGGAGCTGGCGCGTGTGCGCGTCTCTGGGTGC 427
Db 853 ATGCGCTGACGAGGCGCTCAGCTGGGGCGCTGCCGCGTGGCGCGGCTCTCTGGG--- 909
Qy 428 TGGTCATCGGCTCTCTGGTGGCTCTGCTGGGATTCAGAGGGCGGCTTCTGCT 487
Db 910 GGGCACTCTGCTCTCAACGGGCACTGCTCTGACCAACCACTCCAGCGGCTCTGCG 969
Qy 488 TCAG-----GAGCAGCGGCAATTTCACTCCATGCGGTTCCGCTGCTGGGAT 538
Db 970 TCAGTTACAGCTGGGCAAGACCTCGGCTCTCACTAGCTGGGACCAAGGCGCTTGTGG 1029
Qy 539 TCTACCTGCGGCTGGCGTGGTGTCTTCTGCTCCCTGAAGGTGGTGAATGCGCTTGGGCC 598
Db 1030 TGGTGAATCTTCTTGGCGCTGGCGCTCATCTCTTTTGGCTCTGTGAGCATCACGGCA 1089
```





Qy 537 A T T C T A C C T G C C C C T G G C C G T G G T G T T C T G C T C C C T G A A G G T G T G A C T G C C C T 593

Db 853 G G T G G G C T T C G T G T T G T A C A T T T C C T C A T G G G C T T C C T G T G C C C G T C G G G G C C A T 797

## RESULT A

```

US-10-750-623-36071/c
; Sequence 36071, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DeNise, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: WM1100-1
; CURRENT APPLICATION NUMBER: US/10/750,623
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 36071
; LENGTH: 1685
; TYPE: DNA
; ORGANISM: Bovine 19866880675545
US-10-750-623-36071

```

| Query Match           | 9.5%;           | Score 88.2;   | DB 7;     | Length 1685; |
|-----------------------|-----------------|---|-----------|--------------|
| Best Local Similarity | 49.3%;          | Pred. No. 7.4e-09;  |           |              |
| Matches 265;          | Conservative 0; | Mismatches 263;   | Indels 9; | Gaps 1;      |
| QY                    | 66              | CTTCTACGCTPACTTGGCGCTCTGGTGTCTAGGCGCTGTGCTCAACAGCCTGGCGCT     | 125       |              |
| Db                    | 1333            | CATCTCTTTTCACTACTCCGTGGTGTGCTGGTGGGCTCTGTGGGAACCTCCATGGTCA    | 1274      |              |
| QY                    | 126             | CTGGGTGTTCTGCTGCCGATGACAGCAGTGGACGGAGACCCGCATCTPACATGACCAACCT | 185       |              |
| Db                    | 1273            | CTACGTGATCTCGCTACGCCAAGATGAAGACGCCACCAACATCTACATCTCTCAACCT    | 1214      |              |
| QY                    | 186             | GGCGGTGGCCGACCTCTGCGCTGTGTGACCTTGGCCCTTGTGTGTCACATCC-----     | 237       |              |
| Db                    | 1213            | GGCCATGGCCCATGAGCTGCTCATGCTCAGCGTGGCCCTTCTGTGTCACTCCACATGCT   | 1154      |              |
| QY                    | 238             | -CTGGGAGACACTCAGACACGCGCTGTGCCAGCTCTCCACAGGACATCTACCTGACCAA   | 296       |              |
| Db                    | 1153            | TCGCCACTGGCCCTTGGCGCGCTACTCTGCGCGCTCTGTGCTCAGCGTGGACGCGATCAA  | 1094      |              |
| QY                    | 297             | CAGGTACATGAGCATCAGCTGGTCA CGGCCATCGCGTGGACCGCTATGTGGCCGTGCG   | 356       |              |
| Db                    | 1093            | CATGTTACACAGATCTACTGTCTGACTGTGTAGCGTGACCGCTACGTGGCCGTGT       | 1034      |              |
| QY                    | 357             | GCACCCGTGGGTGCCCGCGCTGCGGTCCCGACAGGACGCTGCGCGCGTGTGCGCGGT     | 416       |              |
| Db                    | 1033            | GCACCCCATCAAGCGCGCACGCTACCGCGGCCACCGTGSCCAAGGTGGTGAATCTGGG    | 974       |              |
| QY                    | 417             | CCTCTGGGTGCTGTGATCGGCTCCTGGTGGCTCGCTGGGATTCAGAGAGGG           | 476       |              |
| Db                    | 973             | CGTGTGGGTGCTGCGTGTCTGTCGCCATCGTGTCTCTCGCGCACGGCGGC            | 914       |              |
| QY                    | 477             | CGGCTTCTGCTTCAGAGACCCCGGCACAAATTCACATCCATGGGTTCGCCGTGCTGGG    | 536       |              |
| Db                    | 913             | CAACAGCAGCGACGCTGGCTGTGCAACATGCTCATGCCCGAGCCCGCCACGCTGGCT     | 854       |              |
| QY                    | 537             | ATTCTACTGCCCTGGCGCGTGGTGTCTTCTGTCTCCCTGAAGGTGTGATCTGCCCT      | 593       |              |
| Db                    | 853             | GGTGGGCTTCGTGTTGTACATTTCTCATGGCTTCTGTGCTGCCCGCTCGGGGCAT       | 797       |              |

## RESULT 9

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US-11-127-877-29
; Sequence 29, Application US/11127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Merchiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spittaels, Koenraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; TITLE OF INVENTION: Amyloid-Beta Protein Production
; FILE REFERENCE: P27,800-B USA
; CURRENT APPLICATION NUMBER: US/11/127,877
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/603,948
; PRIOR FILING DATE: 2004-08-24
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 29
; LENGTH: 1077
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-127-877-29

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| Query Match           | 9.1%; Score 84.2; DB 11; Length 1077;                                   |
|-----------------------|---|
| Best Local Similarity | 49.3%; Pred. No. 4.3e-08;   |
| Matches               | 311; Conservative 0; Mismatches 308; Indels 12; Gaps 3;                 |
| Qy                    | 82 GGCCTCTGTGGGCTAGAGCTGCTGCTCAACAGCTGGCGCTCTGGGTGCTTCTGCTGC 141        |
| Db                    | 181 GGAGCCCATCTTCCTGGCAGGCGTGGTGTCAACGGGCTGGCGCTGTAGCTCTTCTGCTGC 240    |
| Qy                    | 142 CGCATGCAGCAGTGGAGCGGACCGCATCTACATGACCAACCTGGCGGTGGCCGACCTC 201      |
| Db                    | 241 CGCACCCGGGCCAAGACACCTCAGTCATCTACACCATCAACCTGGTGGTGACCGATCTA 300     |
| Qy                    | 202 TGCCTGTGTGTCACCTTGTCCTTTCGTGTGTGTCATCTCCCTGGCAGACACTCAGACACGGG 261  |
| Db                    | 301 CTGGTAGGGCTGTCCCTGCCACACGGCTTCGCTGTGTACTACGGCGCCACGGGGTGGCCTG 360   |
| Qy                    | 262 CTGTGCCAGCTCTCCAGGGGATC---TACCTGACCAACAGGTACATGAGCATCAGCCCTG 318    |
| Db                    | 361 CGCTGTGCTCTTCGGCGACGCTCCTCGGTACTTCTCTCAACATGCACTGCTCCATCTCTTTC 420  |
| Qy                    | 319 GTACAGGCCATCGCCGTGGACCGCTATGTGTGGCGGTGGCGCACCCGCTCGTGCCTCCCGCGG 378 |
| Db                    | 421 CTCACCTGCACTGGGTGGACCGCTACTCTGGCCATCGTGGCGCCGAGCTCCCGCCGCC 480      |
| Qy                    | 379 CTGGGTCCCCCAGGACGGCTGCGGCCGTGTGGCGGTCTCTTGGGTGCTGGTCACTGCGC 438     |
| Db                    | 481 TGGCGCAGCTCTGCTGTGCCAGGGCCGTGTGGCGCTTTCGTGTGGCTGGCGCCGGTGGC 540     |
| Qy                    | 439 TCCCTGGTGGTTCGTGGCTCCTGGGGATTTCAGAGGGCGGGTTCGTCTTCAGGAGCACC 498     |
| Db                    | 541 -----GTACCCCTGTGGGTGTGGCGCTGACAGGACGCCGGCCCTGTGCGCGTCTCTT 594       |
| Qy                    | 499 CGGCACAATTTCAACTCATGGGTTCCGGTGTGGGATTCTACTCGCCCTGGCCCGCTG 558       |
| Db                    | 595 GCGCTGACTGTCTGGAGTTCTCTGTGCCCTTCCTGGTGCATCAGCGTG---TTTACCGCG 651    |
| Qy                    | 559 GTGGTCTTCTGCTCCCTGAAGTGTGTGACTGCGCTGGCGCCAGAGGCGCACCCACCGACGTG 618  |
| Db                    | 652 CGCATCATGTGTGCACTGTGCGGCCGGGTCTGCTCCACAGGTCGCGAGCGCCGCGTG 711       |
| Qy                    | 619 GGGCAGGCAGAGGCCACCCGCAAGGCTAAACGATGGTCTGGGCCAACTCTCTGGTGTTC 678     |
| Db                    | 712 CGGGCCATGCAGCTCCTGCTCAGCGTGTCTATCATCTTCTCGTGTCTTACGCGCCTTC 771      |
| Qy                    | 679 GTGGTCTGTTCTGCCCTTCGACGTGGGGC 709                                   |
| Db                    | 772 CACGCCCGCAAGTGGCGGTGGCGCTGTGGC 802                                  |

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; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 32790
; LENGTH: 706
; TYPE: DNA
; ORGANISM: Bovine 19866880843412
US-10-750-185-32790

Query Match      8.0%; Score 74.2; DB 7; Length 706;
Best Local Similarity 51.1%; Pred. No. 3.8e-06;
Matches 203; Conservative 0; Mismatches 188; Indels 6; Gaps 1;

QY 51 AGCGATCAAGCTGGGCTTCTACGCCCTACTTGGGCGTCTGCTAGGCTAGGCTGCTGCT 110
DB 449 AGAGAGCAAGCTGCTTCTTGTCTCTTCTACTGTCATCTTGTATTTGGTCTTCTGGG 390
QY 111 CAACAGCTGGGGCTCTGGGCTTCTGCTGCGCGCATGCGAGCTGAGCGAGACCGGCAT 170
DB 389 CAACAGCTGGTCACTCTAGTCTTGTGCGCTGCAAGAACTGAGAGTGTCAAGATGT 330
QY 171 CTACATGACCAACTGGGCGGTCGACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 230
DB 329 ATACCTCTTGAACCTGGCGCTGCTGACCTGCTTCTTCTTCTTCTTCTTCTTCTTCTGAC 270
QY 231 GCACTCCCTGCGAGAC-----ACCTCAGACAGCGCGCTGCGCAGCTCTCCAGGCGCAT 284
DB 269 CCACTATCAACTGGACAGTGGGTATTCGGGACCGTAATGTGCAAGGTGCTCTCTGGCTT 210
QY 285 CTACCTGACCAACAGGTATGATGAGCATCAGCTGCTGCGGCGCATGCGGCGCATGCGGCGCTA 344
DB 209 TTATTACATGGCTTCTTTCAGCAGCATGCTTCTTATAACCTCATGATGAGACCGGTA 150
QY 345 TGTGGCGGTGGCGACCCCGCTGCGTGGCGCGCGGCTGCGGTCGCCAGGAGGCTGCGGC 404
DB 149 CTTGGCGGTGTCATGCGGTATATGCTTGAAGTGAAGAGCAATCAGCATGGGACAGC 90
QY 405 CTTGTGGCGGTGCTCTGCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTC 441
DB 89 CTTGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 53

RESULT 12
US-10-750-623-32790/c
; Sequence 32790, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: PANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-1
; CURRENT APPLICATION NUMBER: US/10750,623
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 32790
; LENGTH: 706
; TYPE: DNA
; ORGANISM: Bovine 19866880843412
US-10-750-623-32790

Query Match      8.0%; Score 74.2; DB 7; Length 706;
Best Local Similarity 51.1%; Pred. No. 3.8e-06;
Matches 203; Conservative 0; Mismatches 188; Indels 6; Gaps 1;

QY 51 AGCGATCAAGCTGGGCTTCTACGCCCTACTTGGGCGTCTGCTAGGCTAGGCTGCTGCT 110
DB 449 AGAGAGCAAGCTGCTTCTTGTCTCTTCTACTGTCATCTTGTATTTGGTCTTCTGGG 390
QY 111 CAACAGCTGGGGCTCTGGGCTTCTGCTGCGCGCATGCGAGCTGAGCGAGACCGGCAT 170
DB 389 CAACAGCTGGTCACTCTAGTCTTGTGCGCTGCAAGAACTGAGAGTGTCAAGATGT 330
QY 171 CTACATGACCAACTGGGCGGTCGACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 230
DB 329 ATACCTCTTGAACCTGGCGCTGCTGACCTGCTTCTTCTTCTTCTTCTTCTTCTTCTGAC 270
QY 231 GCACTCCCTGCGAGAC-----ACCTCAGACAGCGCGCTGCGCAGCTCTCCAGGCGCAT 284
DB 269 CCACTATCAACTGGACAGTGGGTATTCGGGACCGTAATGTGCAAGGTGCTCTCTGGCTT 210
QY 285 CTACCTGACCAACAGGTATGATGAGCATCAGCTGCTGCGGCGCATGCGGCGCATGCGGCGCTA 344
DB 209 TTATTACATGGCTTCTTTCAGCAGCATGCTTCTTATAACCTCATGATGAGACCGGTA 150
QY 345 TGTGGCGGTGGCGACCCCGCTGCGTGGCGCGCGGCTGCGGTCGCCAGGAGGCTGCGGC 404
DB 149 CTTGGCGGTGTCATGCGGTATATGCTTGAAGTGAAGAGCAATCAGCATGGGACAGC 90
QY 405 CTTGTGGCGGTGCTCTGCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTC 441
DB 89 CTTGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 53

RESULT 11
US-10-750-185-32790/c
; Sequence 32790, Application US/10750185
; Publication No. US200502603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: PANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; 
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